PEPTIDE-ASG_4SG_3 - MHC β CHAIN REGIONS
Linker

FIG. 1A

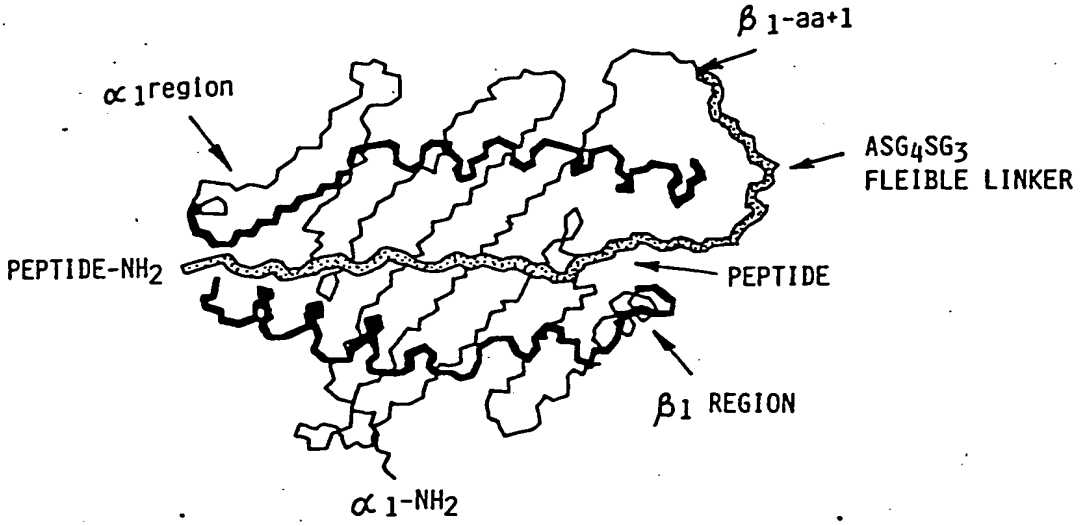


FIG. 1B

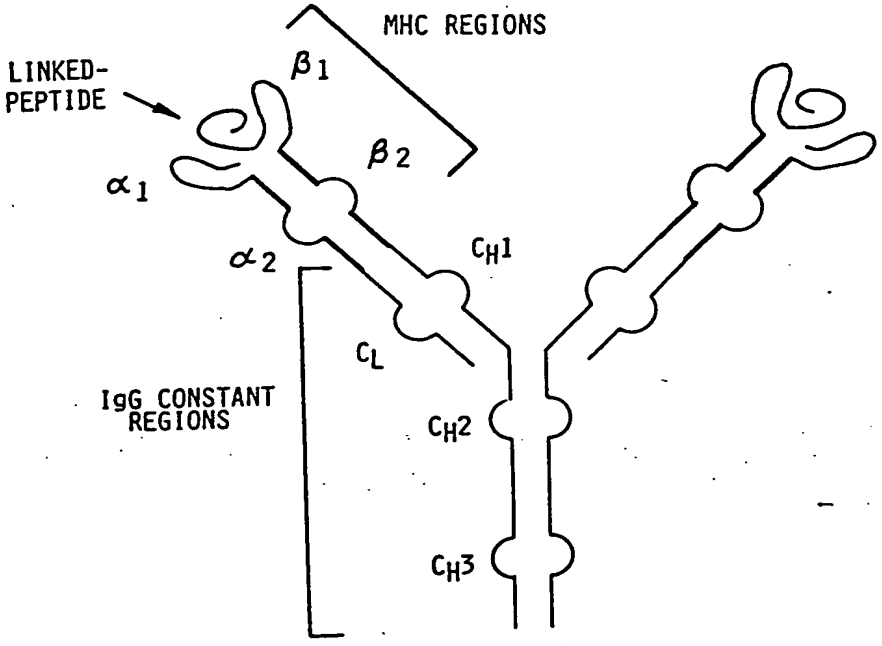


FIG. 1C

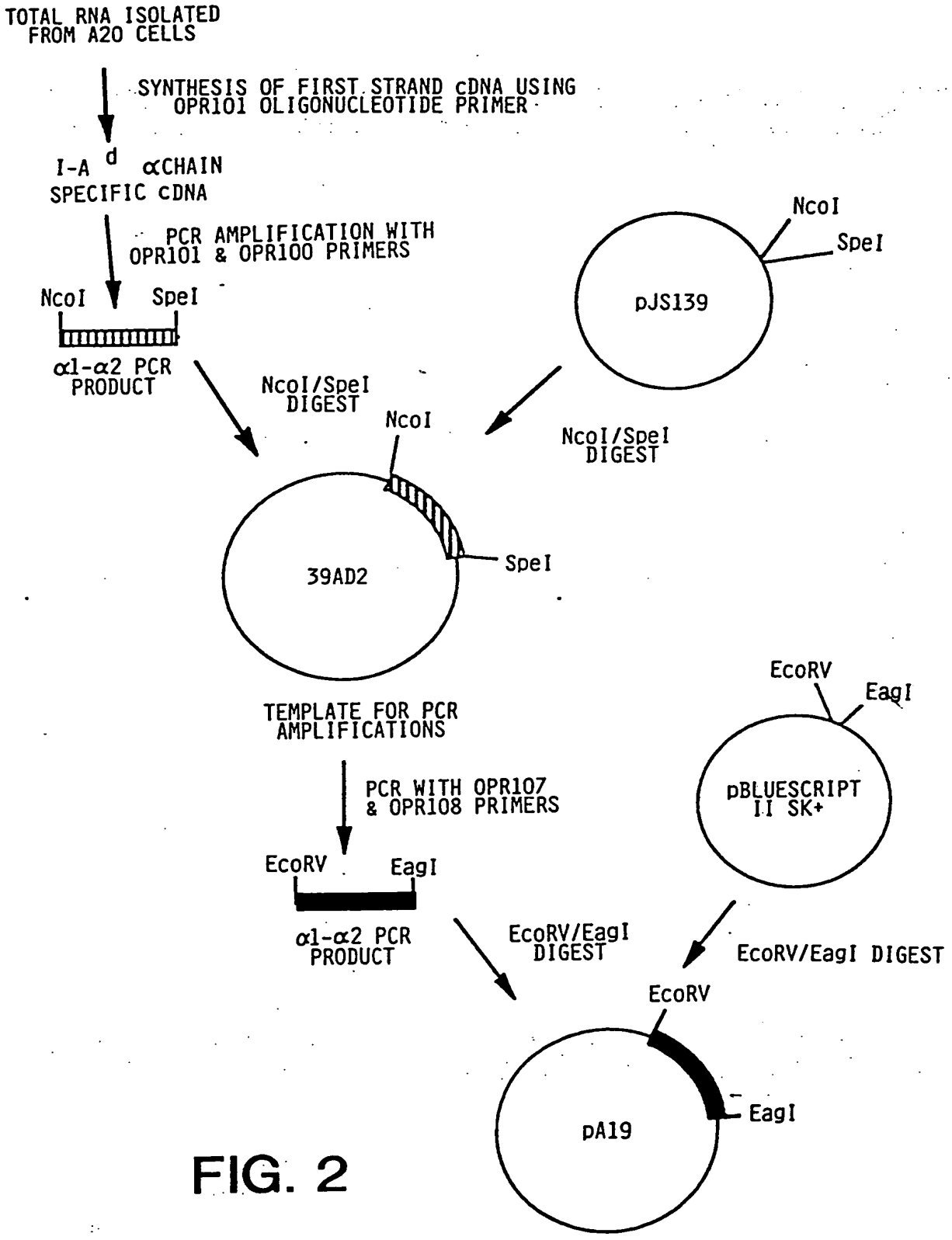


FIG. 2

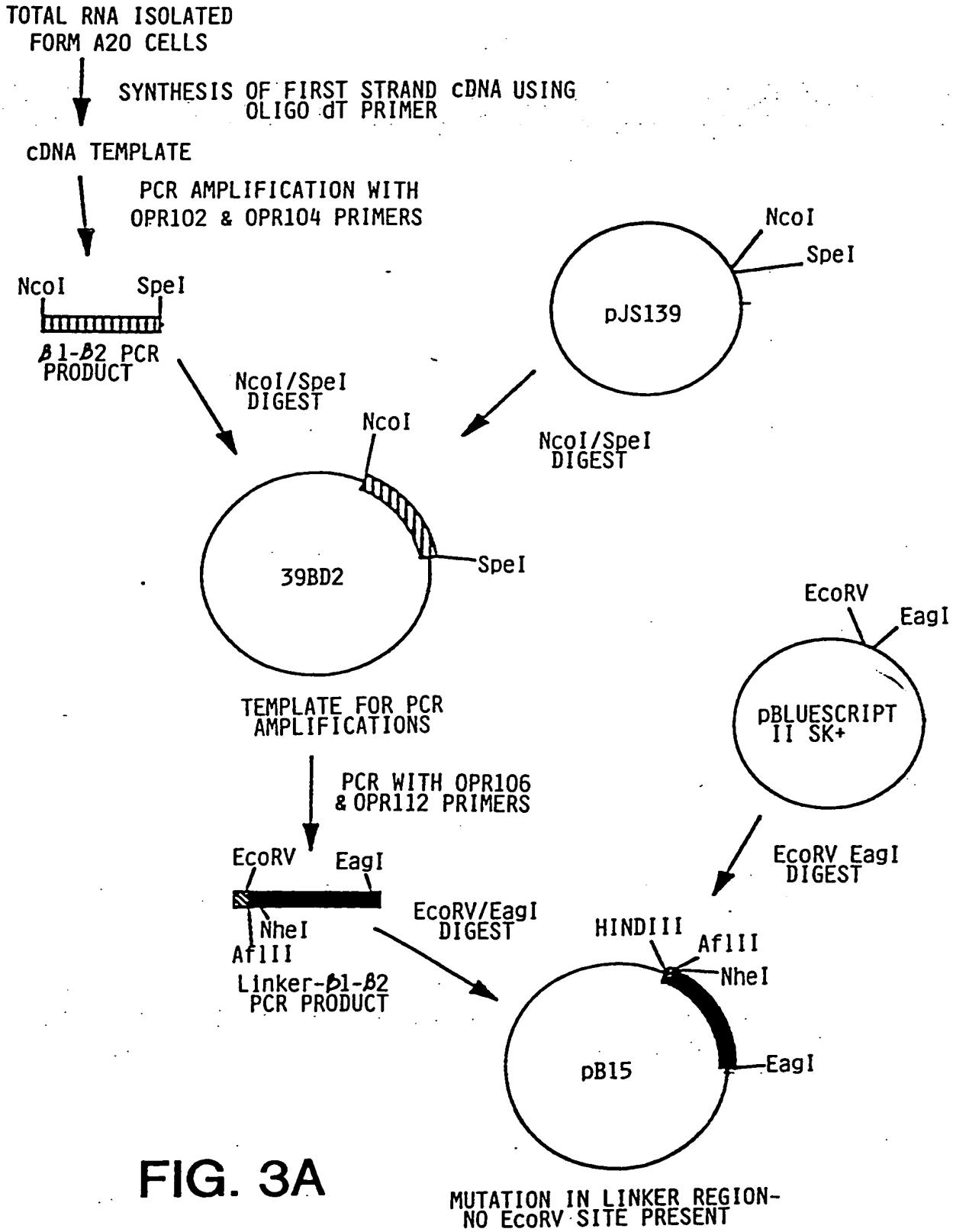


FIG. 3A

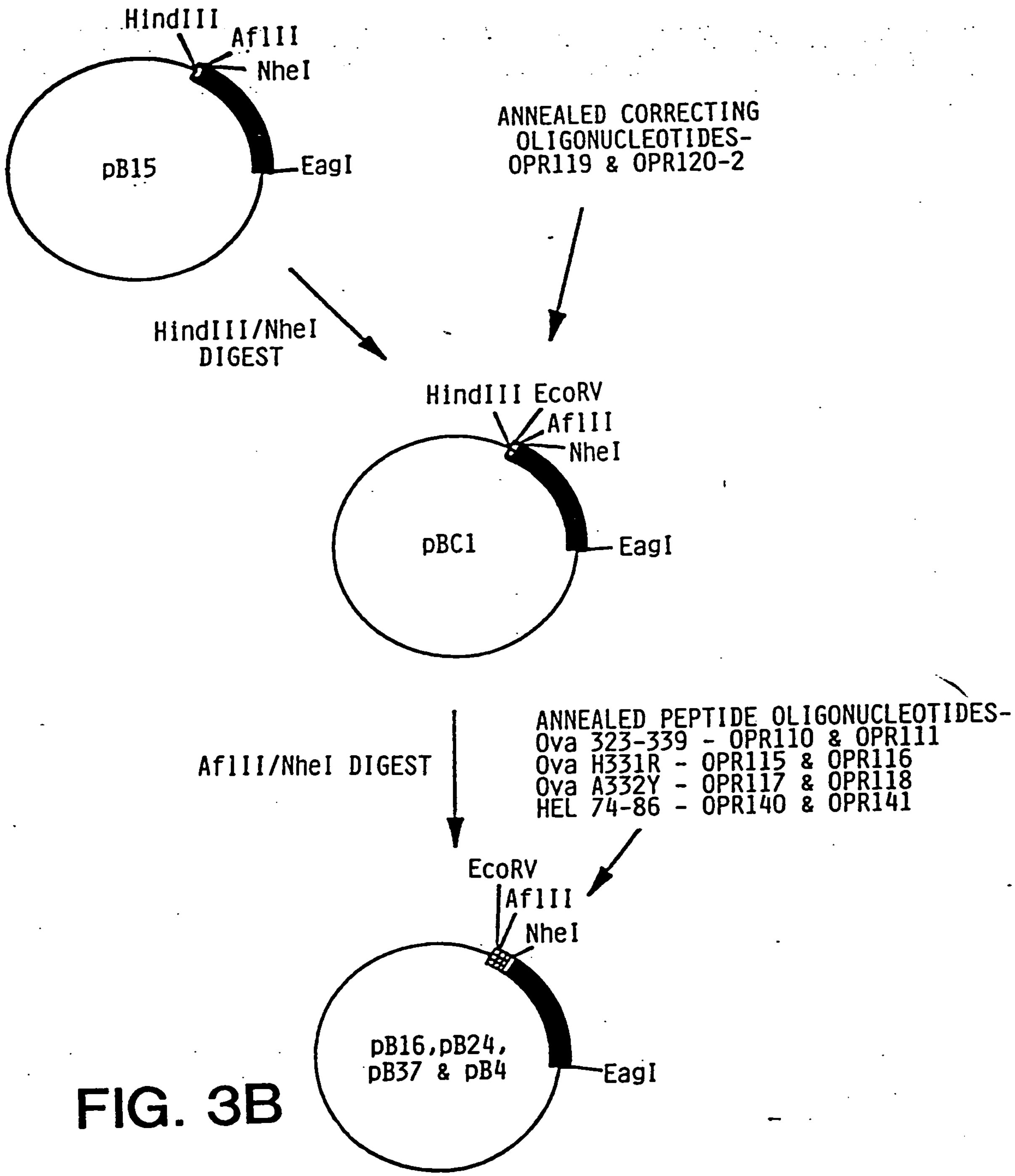

HindIII
AflII
NheI
pB15
EagI
ANNEALED CORRECTING OLIGONUCLEOTIDES- OPR119 & OPR120-2
HindIII/NheI DIGEST
HindIII EcoRV
AflII
NheI
pBC1
EagI
AflII/NheI DIGEST
ANNEALED PEPTIDE OLIGONUCLEOTIDES-
Ova 323-339 - OPR110 & OPR111
Ova H331R - OPR115 & OPR116
Ova A332Y - OPR117 & OPR118
HEL 74-86 - OPR140 & OPR141
EcoRV
AflII
NheI
pB16,pB24, pB37 & pB4
EagI

FIG. 3B

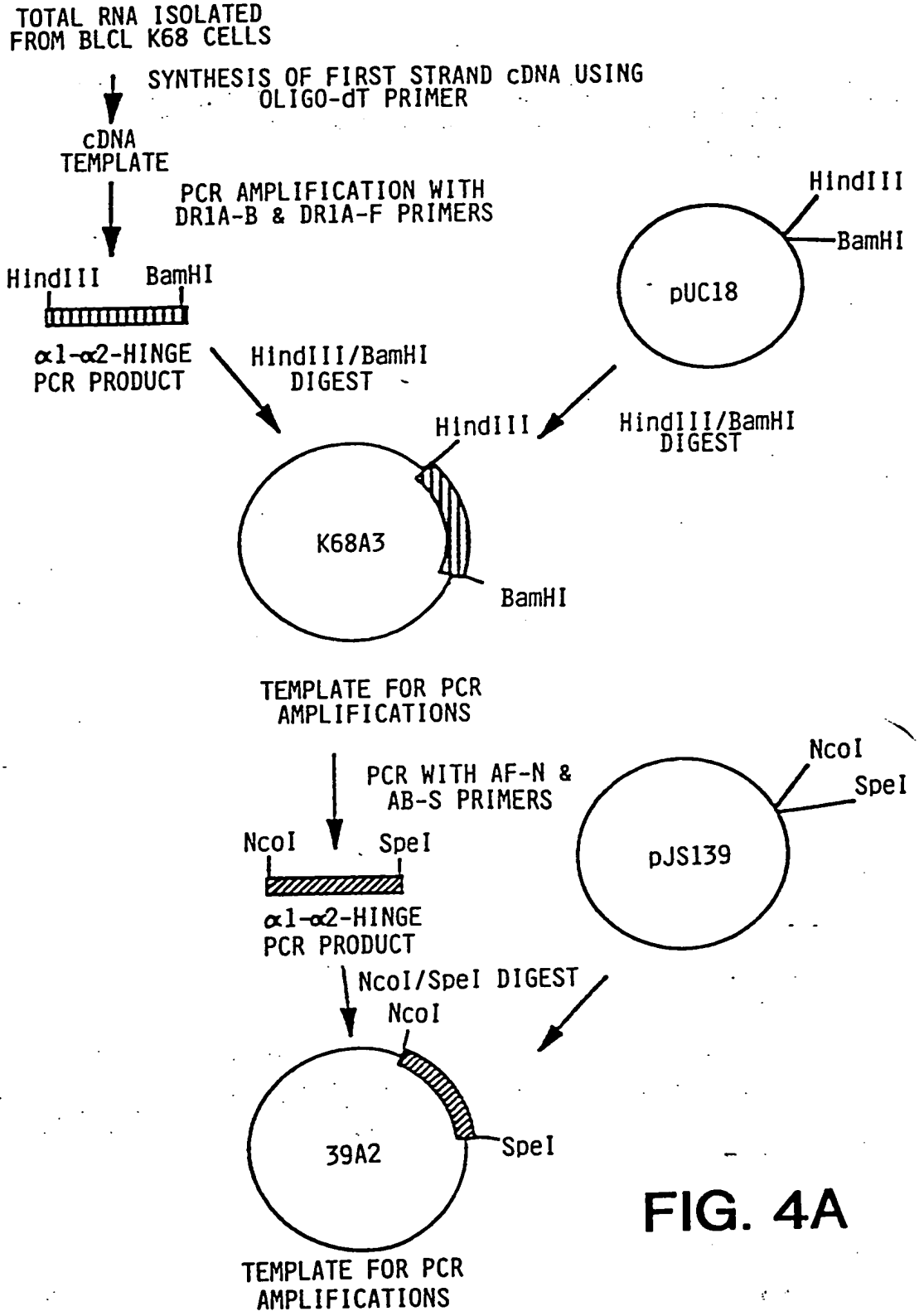


FIG. 4A

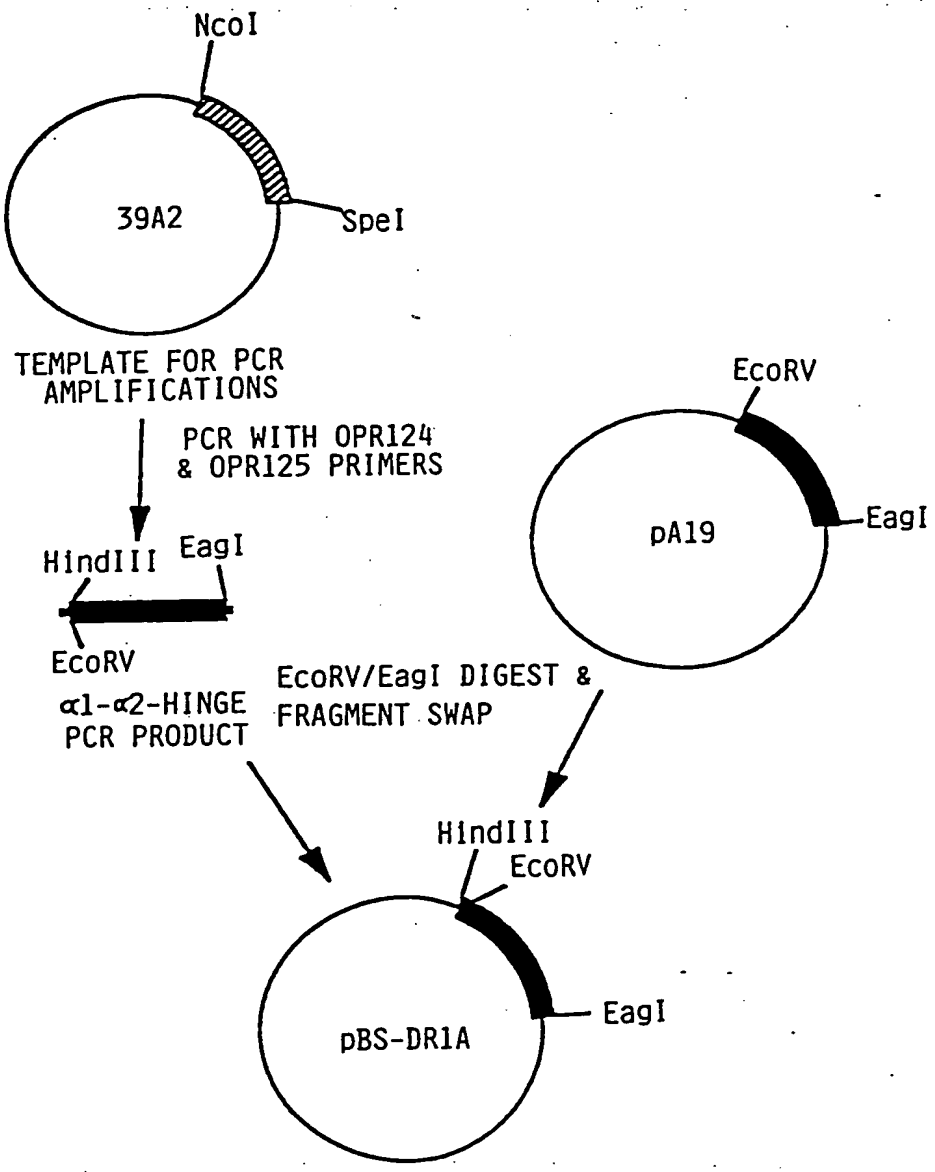


FIG. 4B

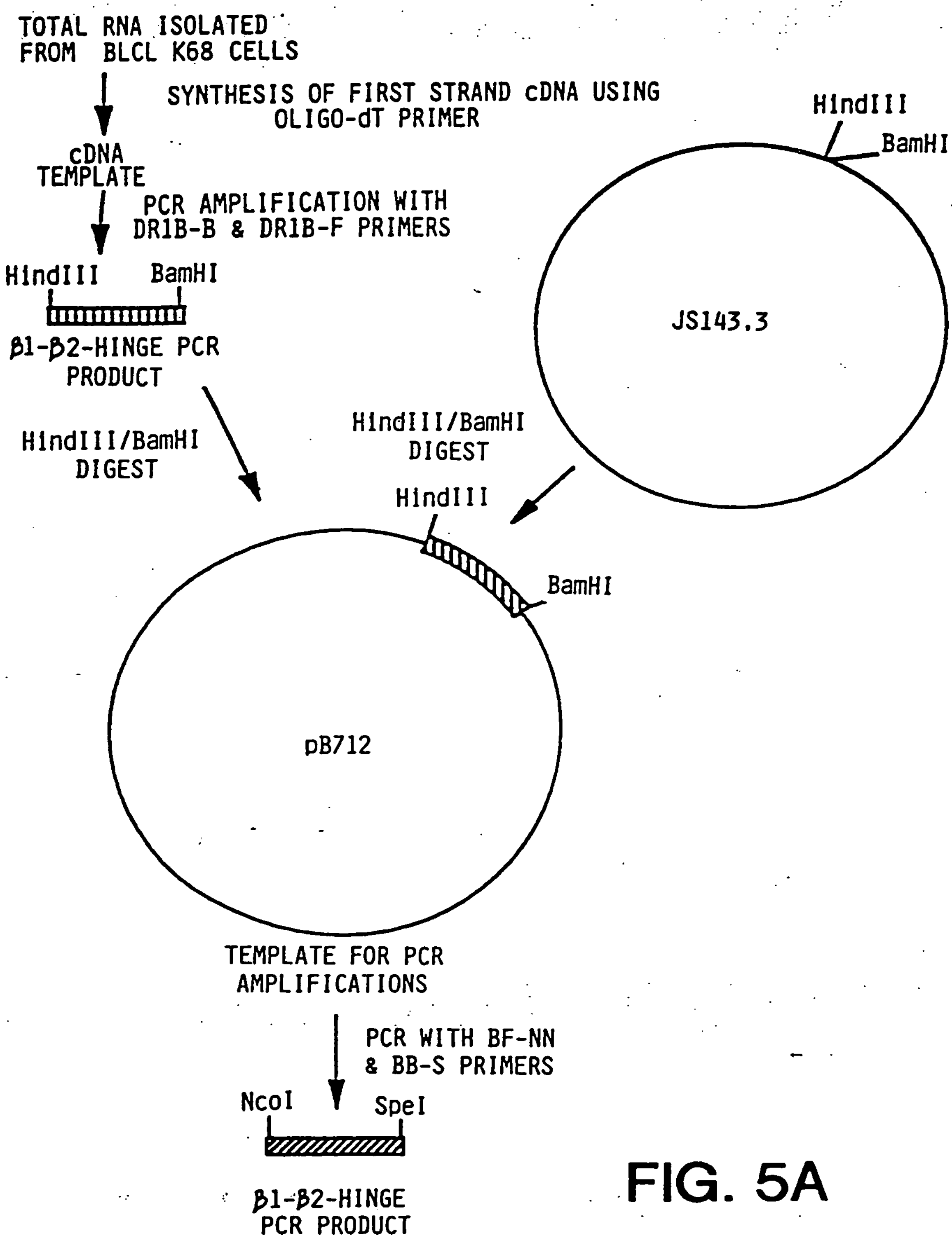


FIG. 5A

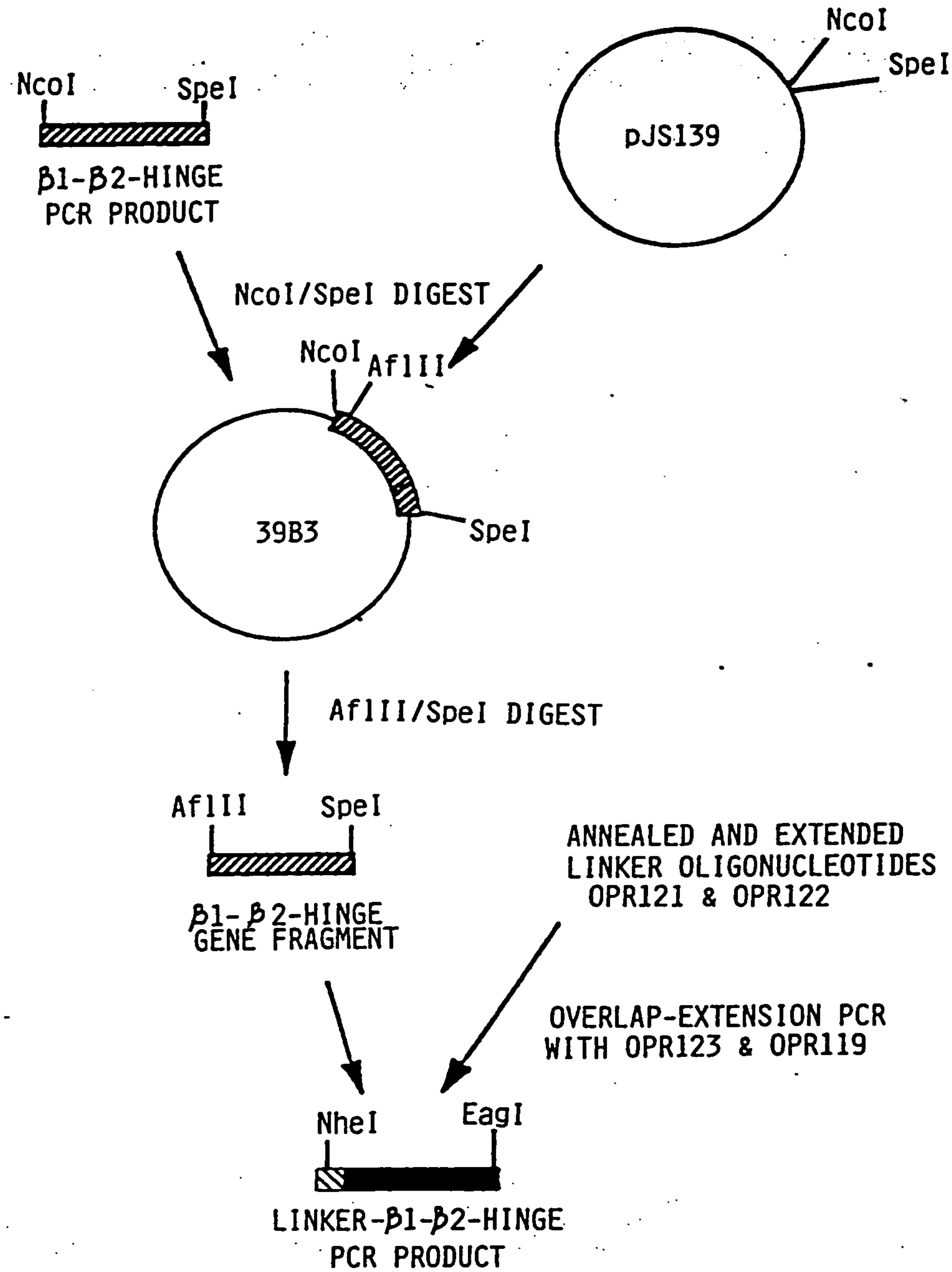


FIG. 5B

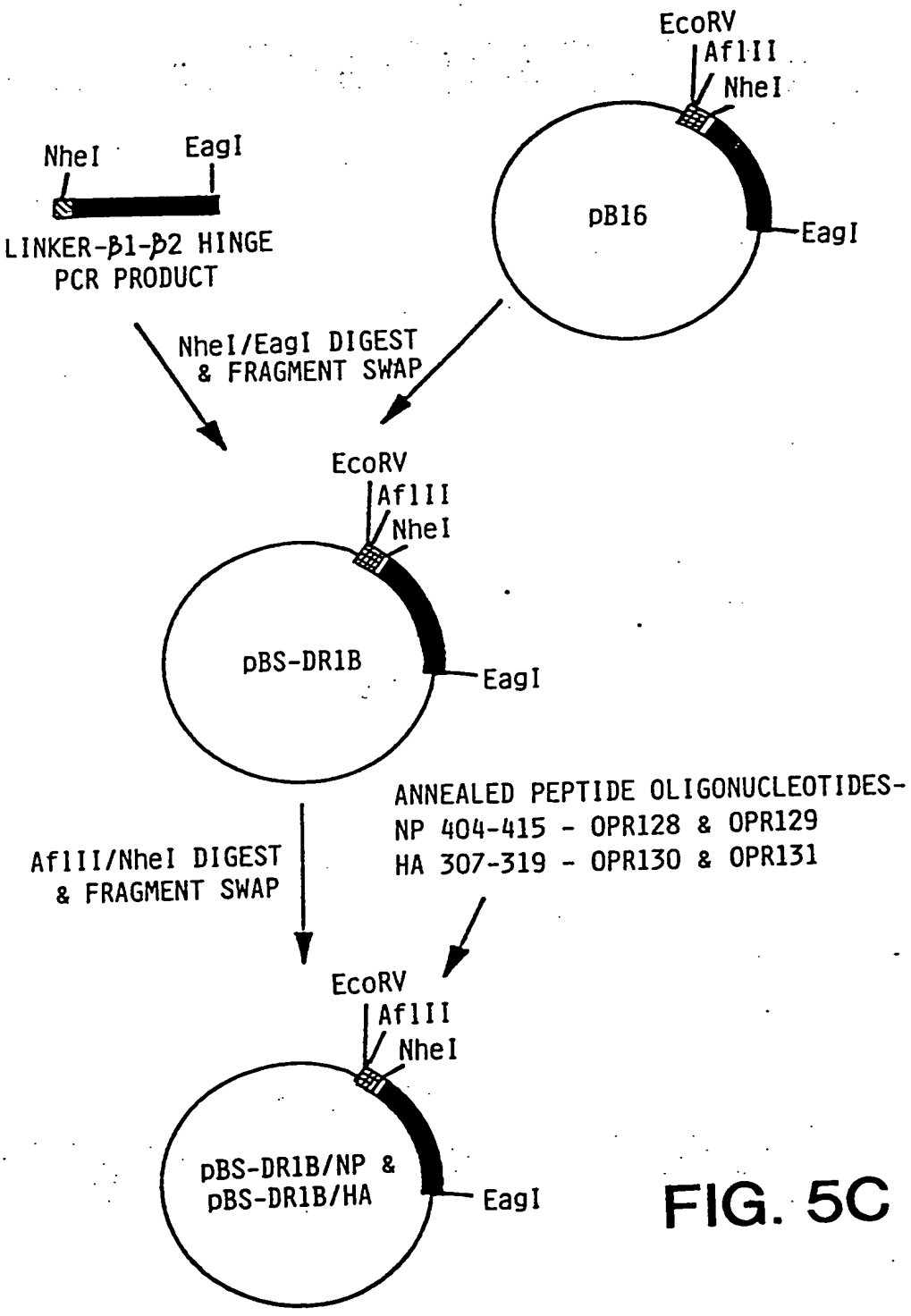


FIG. 5C

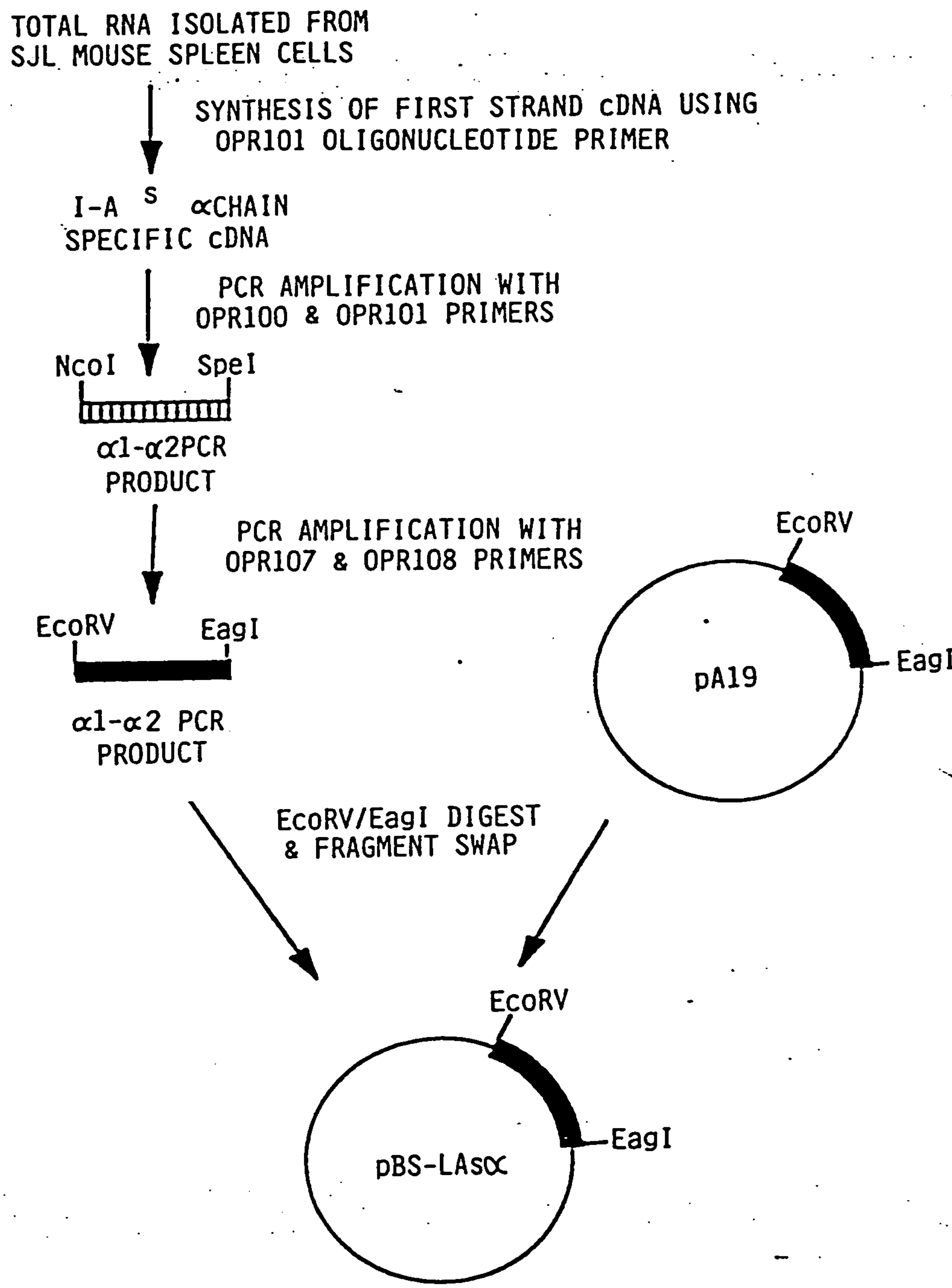

TOTAL RNA ISOLATED FROM
SJL MOUSE SPLEEN CELLS
SYNTHESIS OF FIRST STRAND cDNA USING
OPR101 OLIGONUCLEOTIDE PRIMER
I-A s αCHAIN
SPECIFIC cDNA
PCR AMPLIFICATION WITH
OPR100 & OPR101 PRIMERS
NcoI
SpeI
α1-α2PCR
PRODUCT
PCR AMPLIFICATION WITH
OPR107 & OPR108 PRIMERS
EcoRV
EagI
α1-α2 PCR
PRODUCT
EcoRV
pA19
EagI
EcoRV/EagI DIGEST
& FRAGMENT SWAP
EcoRV
pBS-LAsα
EagI

FIG. 6

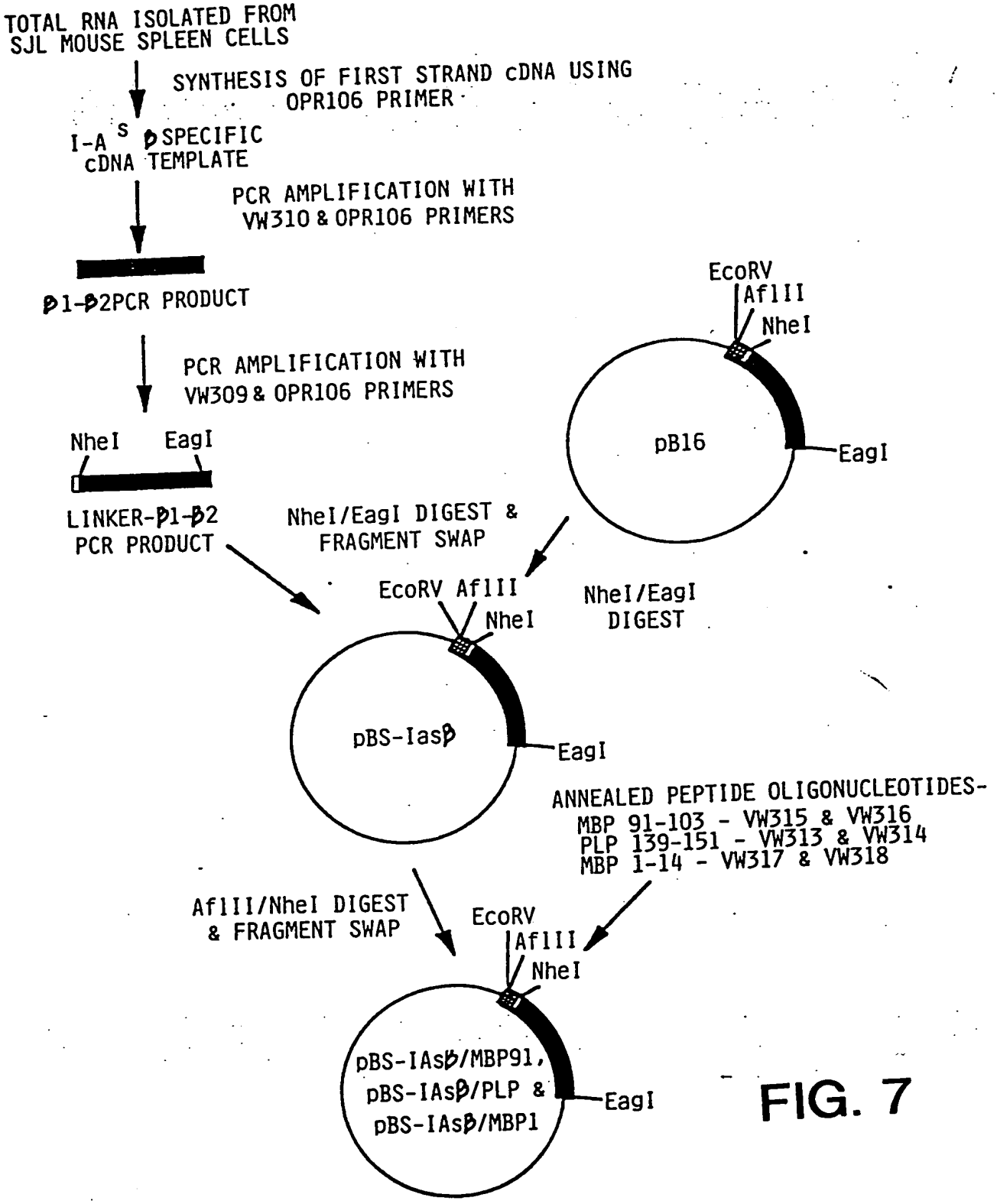


FIG. 7

I-A^{d}/I-A^{s} PCR PRIMERS AND CLONING OLIGONUCLEOTIDES (RESTRICTION SITE ARE UNDERLINED).

OPR100
5'-GGG GGG GCC ATG GCC GAA GAC GAC GAC ATT GAG GCC GAC-3'

OPR101
5'-GCG GCG ACT AGT CCA GTG TTT CAG AAC CGG CTC-3'

OPR107
5'-CCC CCC GAT ATC TCA GCT TCC AGC AGT GGA GAC GAC ATT GAG GCC G-3'

OPR108
5'-CCC CCC CGG CCG CTA CTT ACG TTT CCA GTG TTT CAG AAC CGG C-3'

OPR102
5'-GGG GGG GCC ATG GCC GGA AAC TCC GAA AGG CAT TTC G-3'

OPR104
5'-GCG GCG ACT AGT CCA CTC CAC AGT GAT GGG GC-3'

OPR106
5'-CCC CCC CGG CCG TAC CTG AGG ACC ACT CCA CAG TGA TGG-3'

OPR112
5'-CCC CCC GAT ATC ACA GGT GTC TTA AGT GCT AGC GGA GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC-3'

OPR119
5'-AGC TTG ATA TCA CAG GTG TCT TAA GTG GAG-3'.

OPR120-2
5'-CTA GCT CCA CTT AAG ACA CCT GTG ATA TCA-3'

VW310
5'-TCC GGA GGC GGC GGA GAC TCC GAA AGG CAT TTC G-3'

VW309
5'-CGA TCG CTA GCG GCG GTG GTG GTT CCG GTG GCG GCG GAG-3'

OPR136
5'-CCC CCC AGG CTT CCC GGG CCA CCA TGC CGT GCA GCA GAG CTC TG-3'

OPR139
5'-CCC CCC GAG CTC GAA TTC TCA TAA AGG CCC TGG GTG TCT G-3'

OPR132
5'-CCC CCC AAG CTT CCC GGG CCA CCA TGG CTC TGC AGA TCC CCA GC-3'

OPR133
5'-CCC CCC ACT TAA GGT CCT TGG GCT GCT CAG CAC C-3'

OPR134
5'-CCC CCC CCA TCA CTG TGG AGT GGA GGG-3'

OPR135
5'-CCC CCC GAG CTC GAA TTC TCA CTG CAG GAG CCC TGC TGG-3'

FIG. 8A

HLA-DRI PCR PRIMERS AND CLONING OLIGONUCLEOTIDES.

DRIA-F
5'-GGG GGG AAG CTT ATG ATC AAA GAA GAA CAT GTG ATC ATC-3'

DRIA-B
5'-GCG GCG GGA TCC GTT CTC TGT AGT CTC TGG GAG AGG-3'

DRIB-F
5'-GGG GGG AAG CTT ATG GGG GAC ACC CGA CCA CGT TTC TTG TGG CAG C-3'

AF-N
5'-GGG GGG GCC ATG GCC ATC AAA GAA GAA CAT GTG ATC ATC-3'

AB-S
5'-GCG GCG ACT AGT GTT CTC TGT AGT CTC TGG GAG AGG-3'

OPR124
5'-GGG GGG AAG CTT GAT ATC TCA GCT TCC AGC AGT AGT ATC AAA GAA GAA CAT GTG ATC-3'

OPR125
5'-GGG GGG CGG CCG CTA CTT ACG TTT CTC TGG GAG AGG GCT TGG AGC-3'

DRIB-B
5'-GCG GCG GGA TCC CTT GCT CTG TGC AGA TTC AGA CC-3'

BF-NN
5'-GGG GGG GCC ATG GCC GGA TCC GCT AGC GGG GAC ACC CGA CCA CGT TTC TTG-3'

BB-S
5'-GCG GCG ACT AGT CTT GCT CTG TGC AGA TTC AGA CCG-3'

OPR121
5'-GTT GTC TTA AGT GGA GCT AGC GGA GGG GGC GGG TCC GGA GGT GGT GGG GAC ACC CG-3'

OPR122
5'-GAA ATG ACA TTC AAA CTT CAG CTG CCA CAA GAA ACG TGG TCG GGT GTC CCC ACC ACC-3'

OPR123
5'-GGG GGG CGG CCG TAC CTG AGG ACT TGC TCT GTG CAG ATT CAG-3'

FIG. 8B

PEPTIDE OLIGONUCLEOTIDES.

Ova 323-339
OPR110
5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT G-3'

OPR111
5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA GCC TGA GCA GCG TGA ACA GCC TGA GAG ATA C-3'

Ova H331R
OPR115
5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CGG GCT GAA ATC AAC GAA GCT GGT CGT G-3'

OPR116
5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA GCC CGA GCA GCG TGA ACA GCC TGA GAG ATA C-3'

Ova A332Y
OPR117
5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CAC TAC GAA ATC AAC GAA GCT GGT CGT G-3'

OPR116
5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA TAG TGA GCA GCG TGA ACA GCC TGA GAG ATA C-3'

HEL 74-86
OPR140
5'-TTA AGT AAC CTG TGC AAC ATC CCC TGC AGC GCC CTG CTG AGC TCC G-3'

OPR141
5'-CTA GCG GAG CTC AGC AGG GCG CTG CAG GGG ATG TTG CAC AGG TTA C-3'

NP 404-415
OPR128
5'-TTA AGT CAG ATC AGC GTG CAG CCC GCC TTC AGC GTG CAG G-3'

FIG. 8C

OPR129
5'-CTA GCC TGC ACG CTG AAG GCG GGC TGA ACG CTG ATC TGA C-3'

HA 307-319
OPR130
5'-TTA AGT CCC AAG TAC GTG AAG CAG AAC ACC CTG AAG CTG GCC ACC G-3'

OPR131
5'-CTA GCG GTG GCC AGC TTC AGG GTG TTC TGC TTC ACG TAC TTG GGA C-3'

MBP 91-103
VW315
5'-TTA AGT CAC TAT GGC TCC CTG CCG CAG AAG TCC CAG CAC GGG CGC G-3'

VW316
5'-CTA GCG CGC CCG TGC TGG GAC TTC TGC GGC AGG GAG CCA TAG TGA C-3'

PLP 139-151
VW313
5'-TTA CAT CAC TCC CTG GGC AAG TGG CTG GGC CAC CCG GAC AAG TTC G-3'

VW314
5'-CTA GCG AAC TTG TTC GGG TGG CCC AGC CAC TTG CCC AGG GAG TGA C-3'

MBP 1-14
VW317
5'-TTA AGT ATG GCA TCC CAG AAG CGC CCG TCC CAG CGC TCC AAG TAC CTG G-3'

VW316
5'-CTA GCC AGG TAC TTG GAG CGC TGG GAC GGG CGC TTC TGG GAT GCC ATA C-3'

FIG. 8D

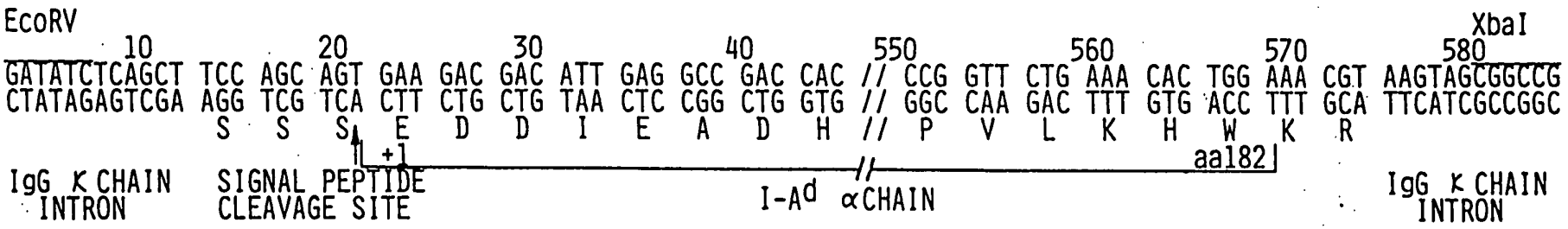

EcoRV
XbaI
10 20 30 40 550 560 570 580
GATATCTCAGCT TCC AGC AGT GAA GAC GAC ATT GAG GCC GAC CAC // CCG GTT CTG AAA CAC TGG AAA CGT AAGTAGCGGCCG
CTATAGAGTCGA AGG TCG TCA CTT CTG CTG TAA CTC CGG CTG GTG // GGC CAA GAC TTT GTG ACC TTT GCA TTCATCGCCGGC
S S S E D D I E A D H // P V L K H W K R
+1
aa182
IgG κ CHAIN INTRON
SIGNAL PEPTIDE CLEAVAGE SITE
I-Ad αCHAIN
IgG κ CHAIN INTRON

FIG. 9A

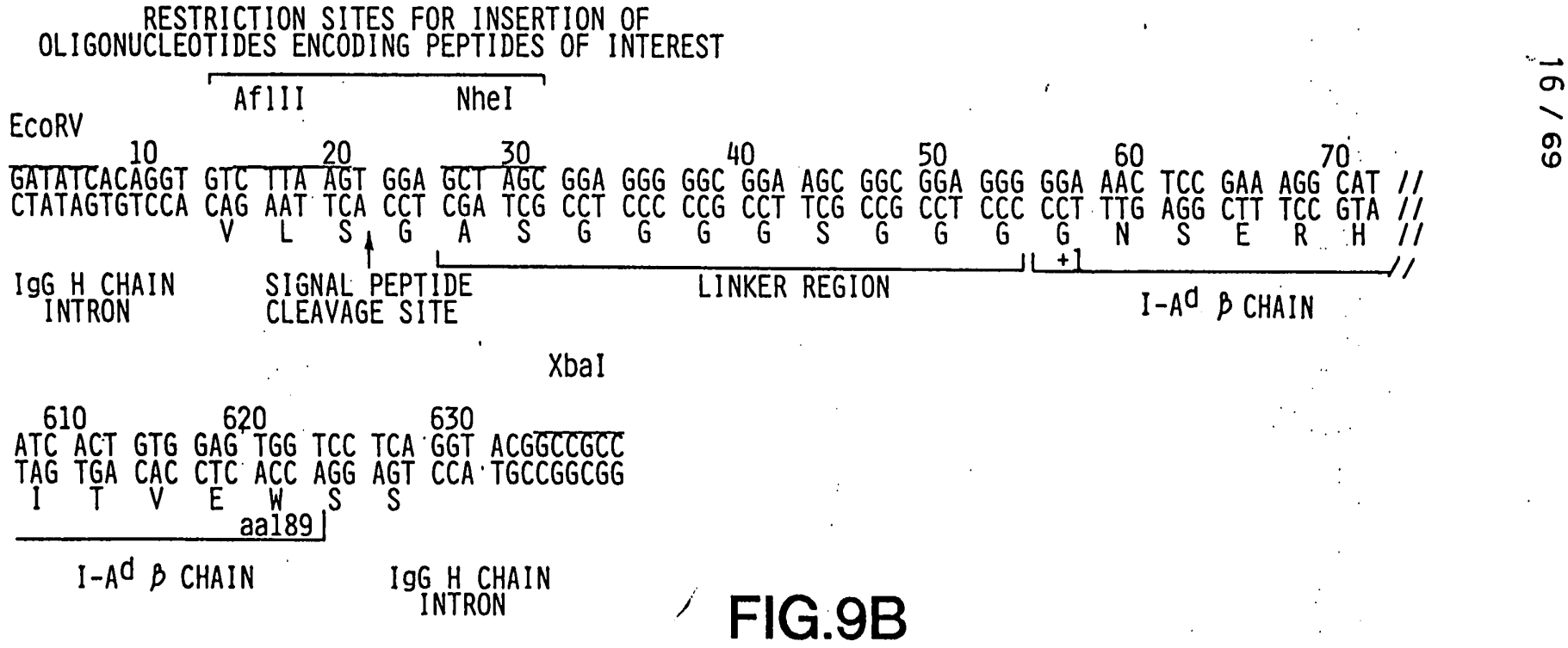

RESTRICTION SITES FOR INSERTION OF OLIGONUCLEOTIDES ENCODING PEPTIDES OF INTEREST
AflII
NheI
EcoRV
10 20 30 40 50 60 70
GATATCACAGGT GTC TTA AGT GGA GCT AGC GGA GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT //
CTATAGTGTCCA CAG AAT TCA CCT CGA TCG CCT CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA //
V L S G A S G G G G S G G G G N S E R H //
+1
IgG H CHAIN INTRON
SIGNAL PEPTIDE CLEAVAGE SITE
LINKER REGION
I-Ad β CHAIN
XbaI
610 620 630
ATC ACT GTG GAG TGG TCC TCA GGT ACGGCCGCC
TAG TGA CAC CTC ACC AGG AGT CCA TGCCGGCGG
I T V E W S S
aa189
I-Ad β CHAIN
IgG H CHAIN INTRON

FIG.9B

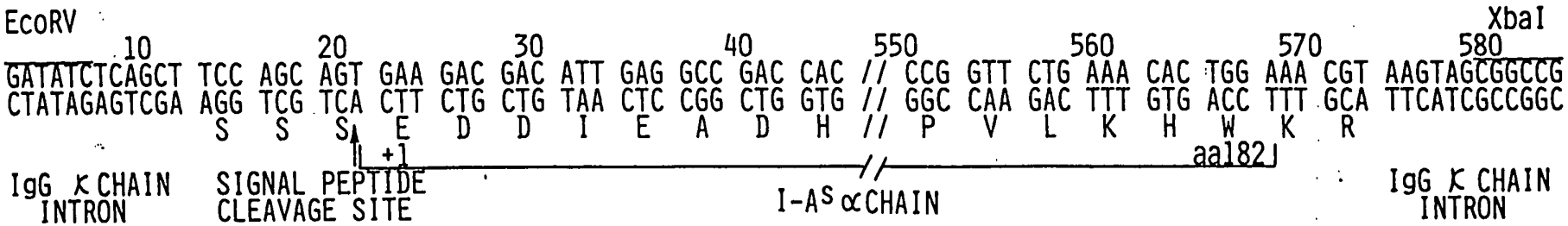

EcoRV
XbaI
10 20 30 40 550 560 570 580
GATATCTCAGCT TCC AGC AGT GAA GAC GAC ATT GAG GCC GAC CAC // CCG GTT CTG AAA CAC TGG AAA CGT AAGTAGCGGCCG
CTATAGAGTCGA AGG TCG TCA CTT CTG CTG TAA CTC CGG CTG GTG // GGC CAA GAC TTT GTG ACC TTT GCA TTCATCGCCGGC
S S S E D D I E A D H // P V L K H W K R
+1
aa182
IgG κ CHAIN INTRON
SIGNAL PEPTIDE CLEAVAGE SITE
I-A^{S} αCHAIN
IgG κ CHAIN INTRON

FIG. 9C

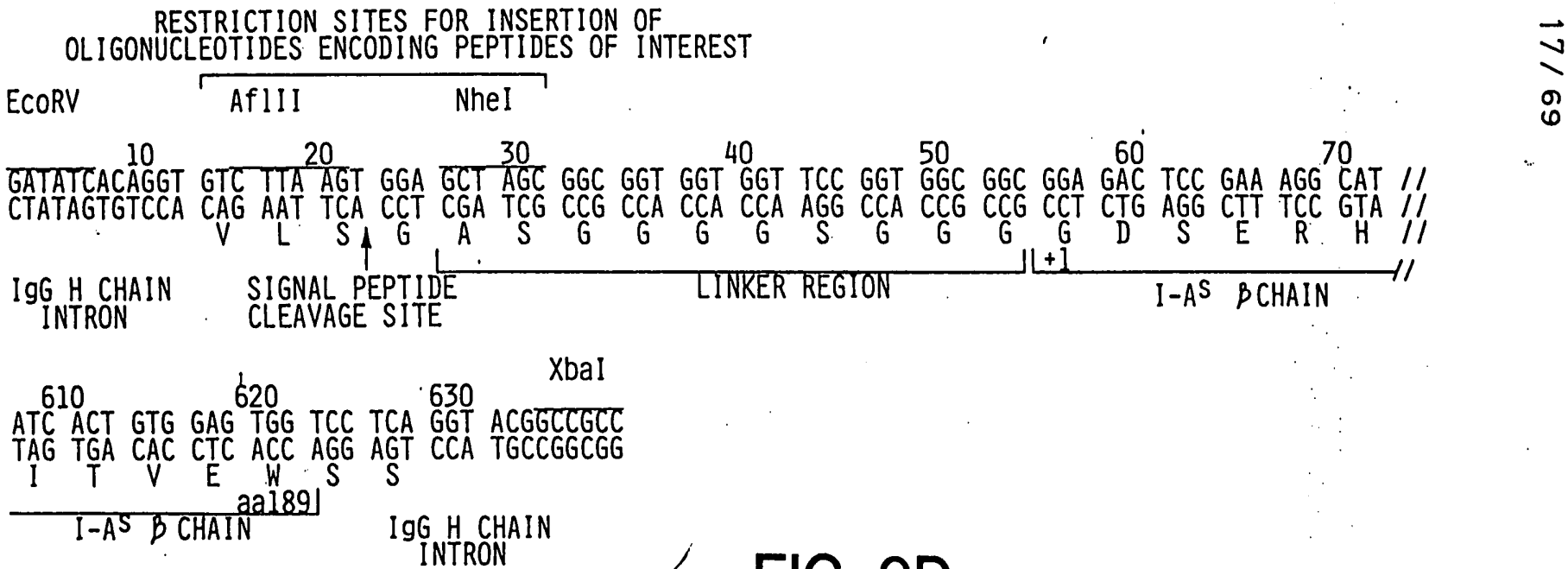

RESTRICTION SITES FOR INSERTION OF
OLIGONUCLEOTIDES ENCODING PEPTIDES OF INTEREST
EcoRV
AflII
NheI
10 20 30 40 50 60 70
GATATCACAGGT GTC TTA AGT GGA GCT AGC GGC GGT GGT GGT TCC GGT GGC GGC GGA GAC TCC GAA AGG CAT //
CTATAGTGTCCA CAG AAT TCA CCT CGA TCG CCG CCA CCA CCA AGG CCA CCG CCG CCT CTG AGG CTT TCC GTA //
V L S G A S G G G G S G G G G D S E R H //
+1
IgG H CHAIN INTRON
SIGNAL PEPTIDE CLEAVAGE SITE
LINKER REGION
I-A^{S} βCHAIN
XbaI
610 620 630
ATC ACT GTG GAG TGG TCC TCA GGT ACGGCCGCC
TAG TGA CAC CTC ACC AGG AGT CCA TGCCGGCGG
I T V E W S S
aa189
I-A^{S} βCHAIN
IgG H CHAIN INTRON

FIG. 9D

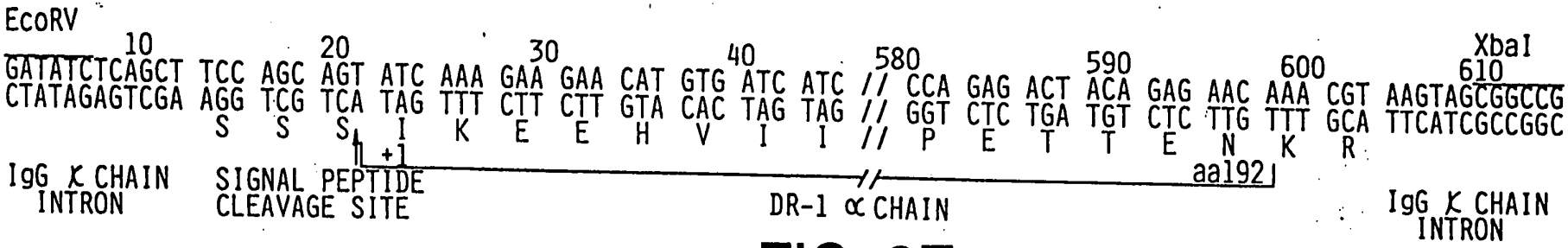


FIG. 9E

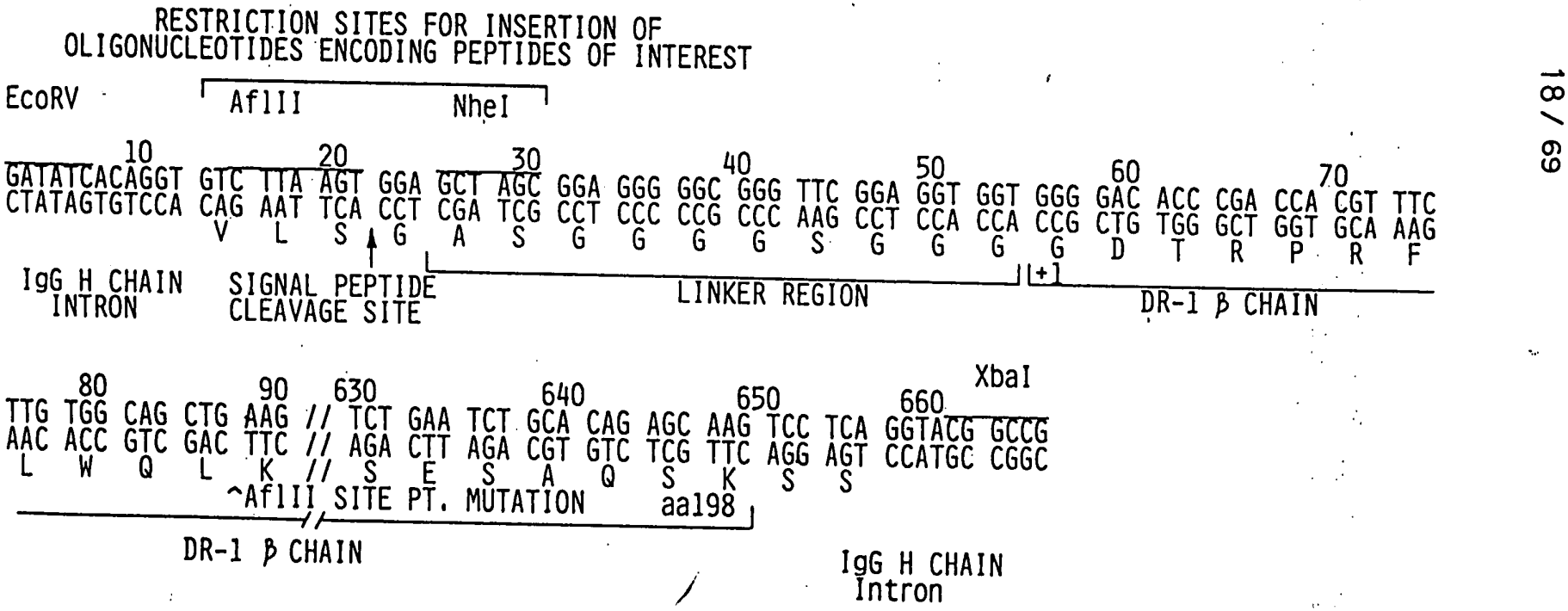


FIG. 9F

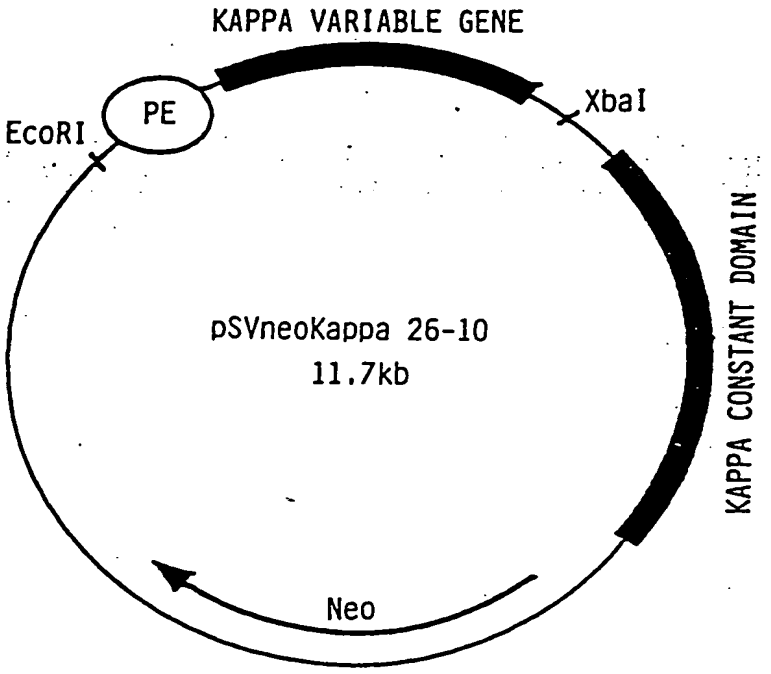


FIG. 10A

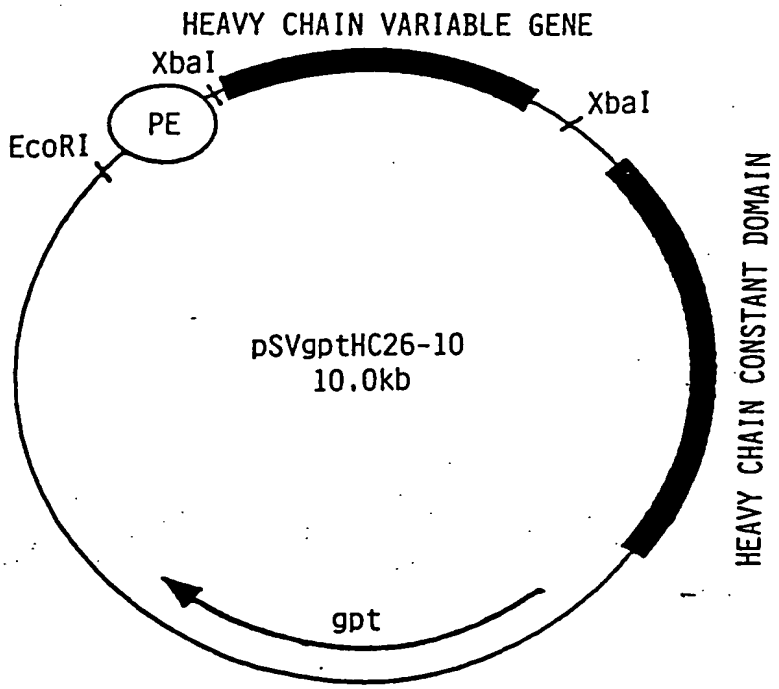


FIG. 10B

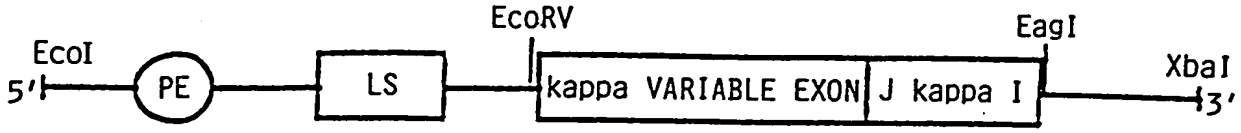


FIG. 11A

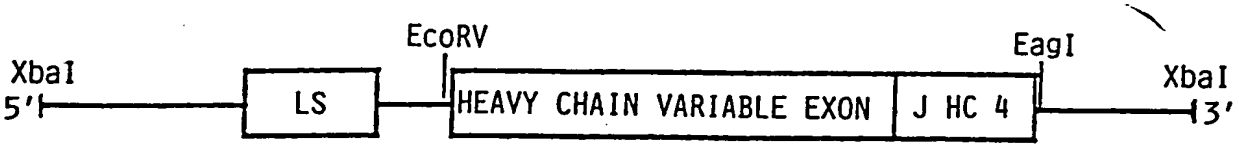


FIG. 11B

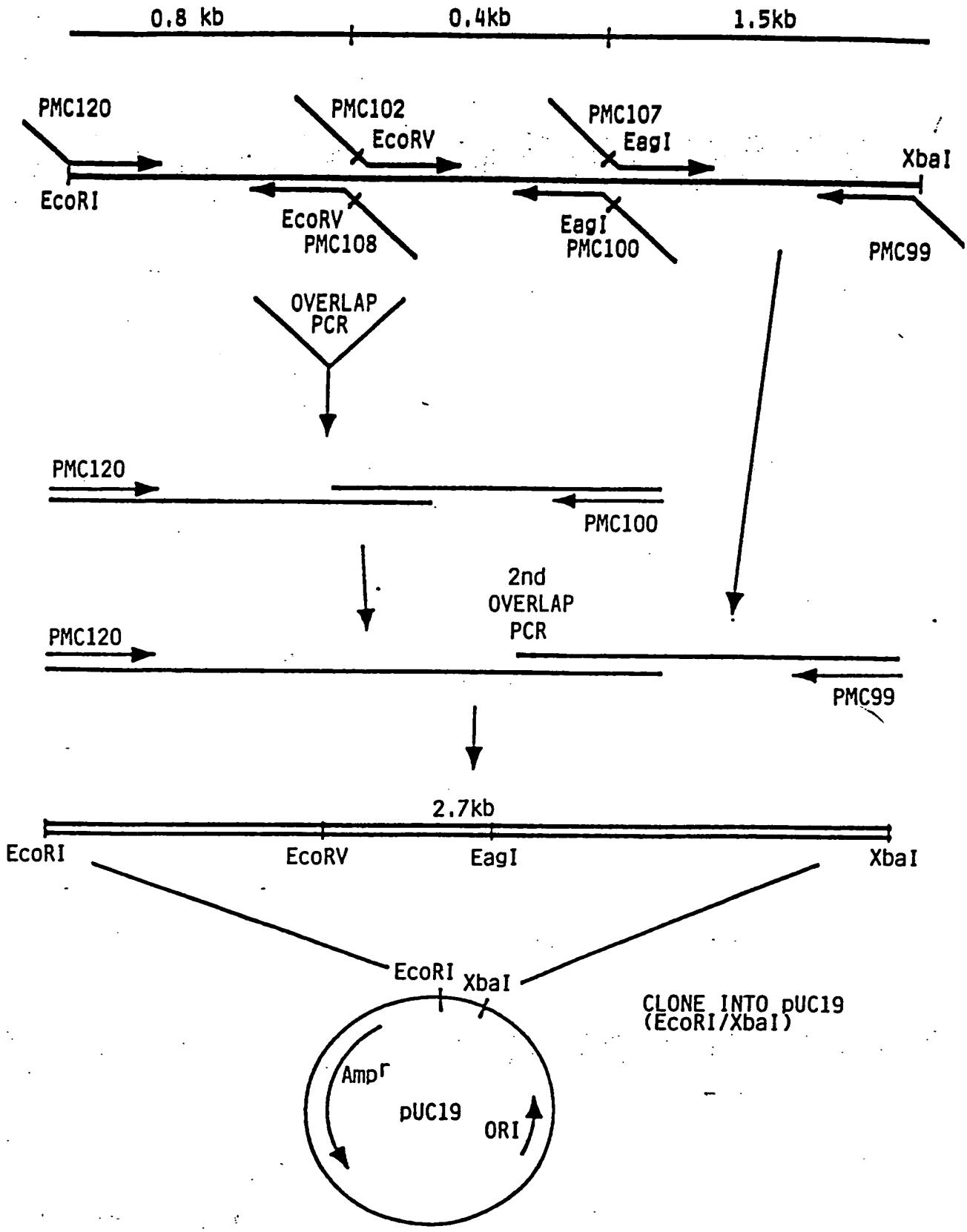

0.8 kb
0.4kb
1.5kb
PMC120
PMC102
EcoRV
PMC107
EagI
XbaI
EcoRI
EcoRV
PMC108
EagI
PMC100
PMC99
OVERLAP
PCR
PMC120
PMC100
2nd
OVERLAP
PCR
PMC120
PMC99
2.7kb
EcoRI
EcoRV
EagI
XbaI
EcoRI
XbaI
CLONE INTO pUC19
(EcoRI/XbaI)
Amp
pUC19
ORI

FIG. 12

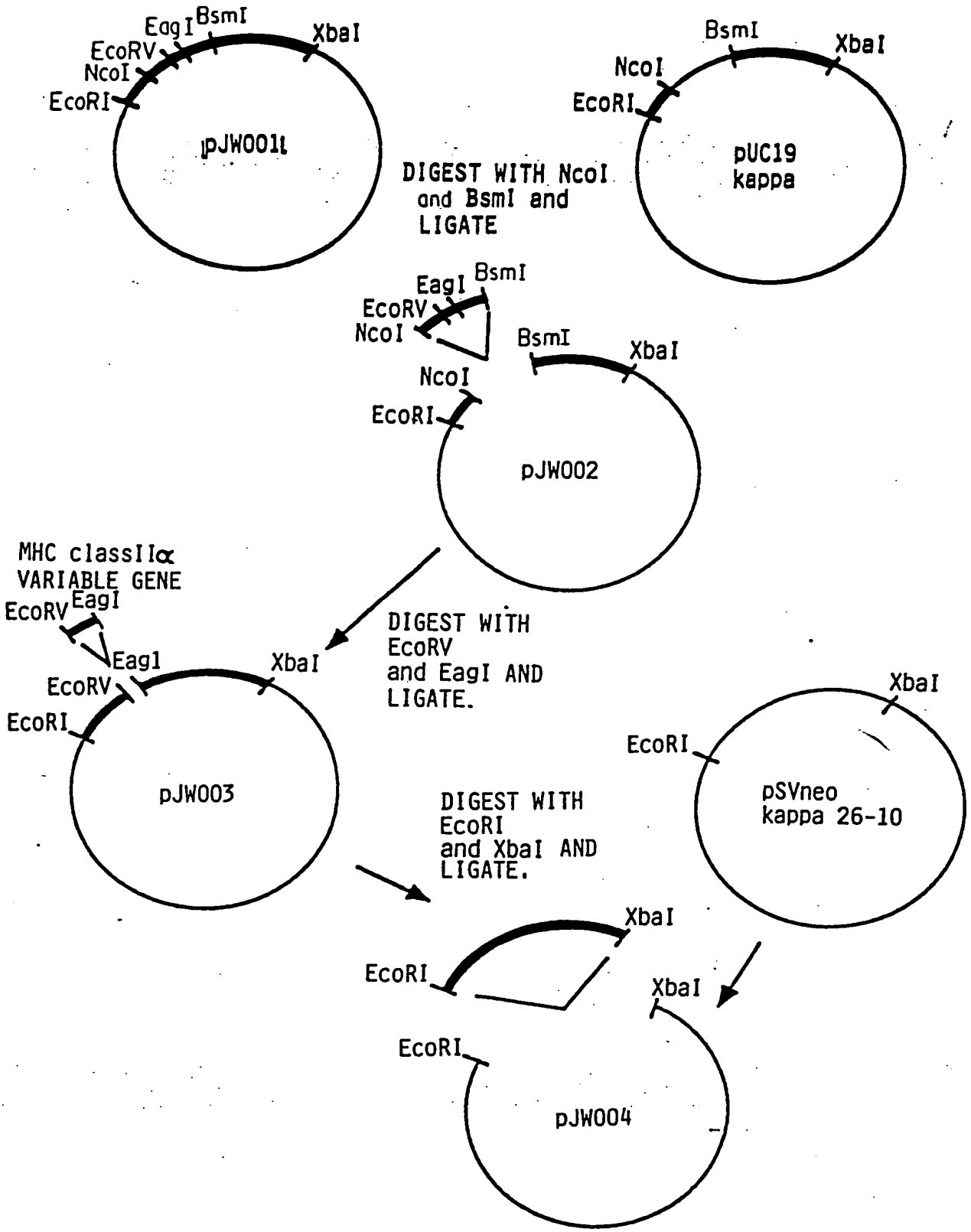


FIG. 13

PRIMER LIST	SEQUENCE
PMC-33	[5'GCTCAGCTGTCTTGTTTCAGTACTGATC3']
PMC-77	[5'GTAAGTAGCGGCCG3']
PMC-111	[5'GGTATGTAAAAATAAACATCACAG3']
PMC-114	[5'GCTTTGCTTACGGAGTTACTC3']

FIG. 14

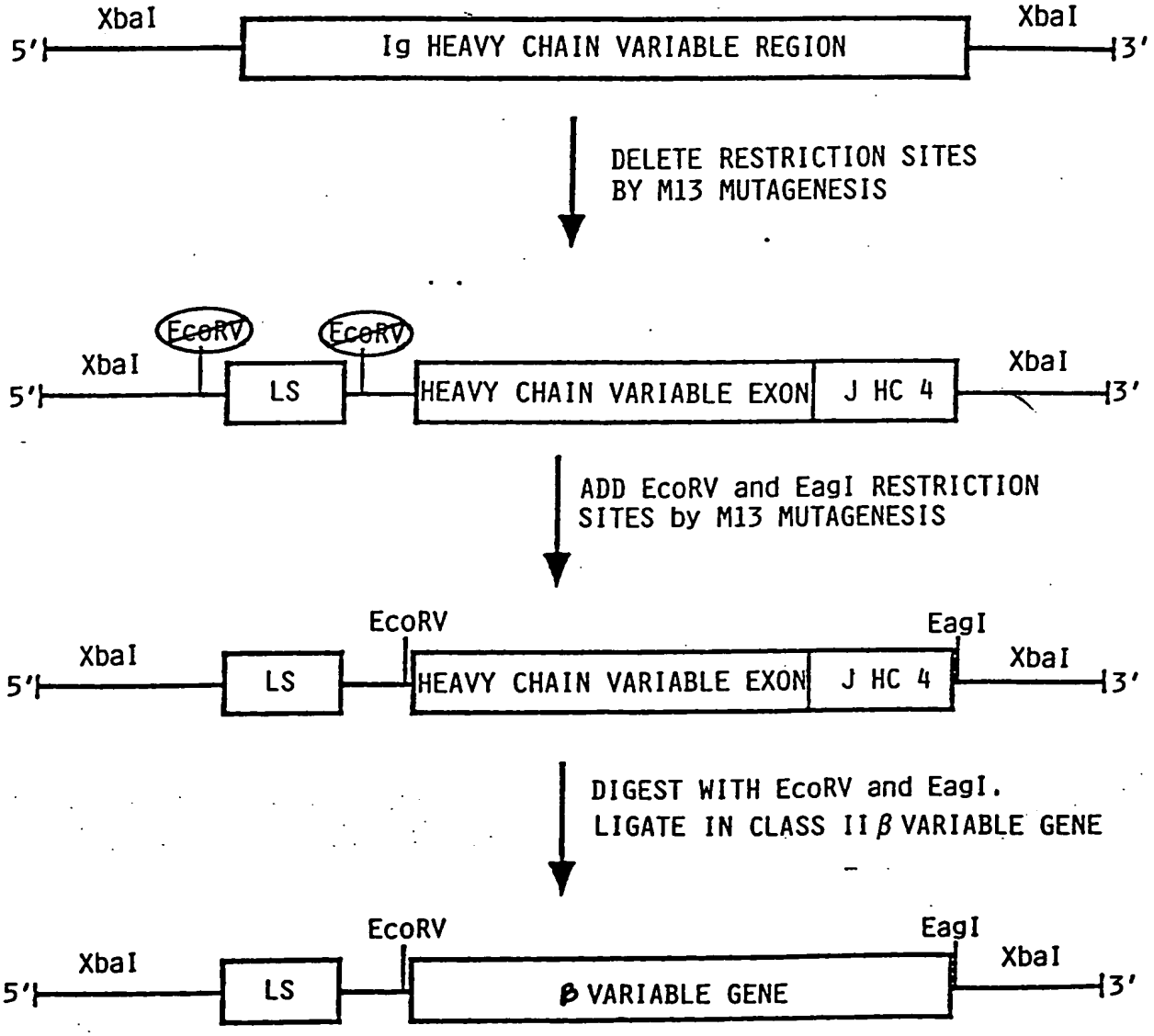


FIG. 15

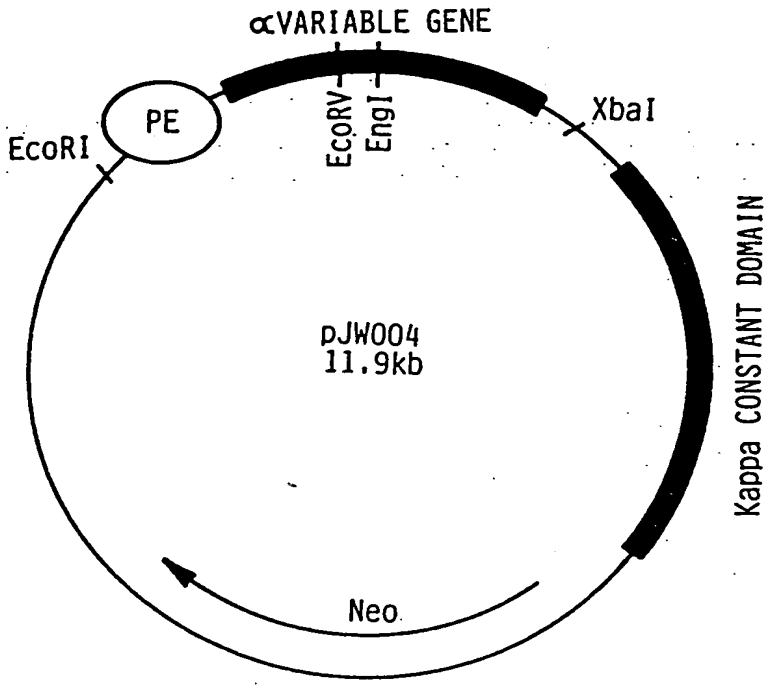


FIG. 16A

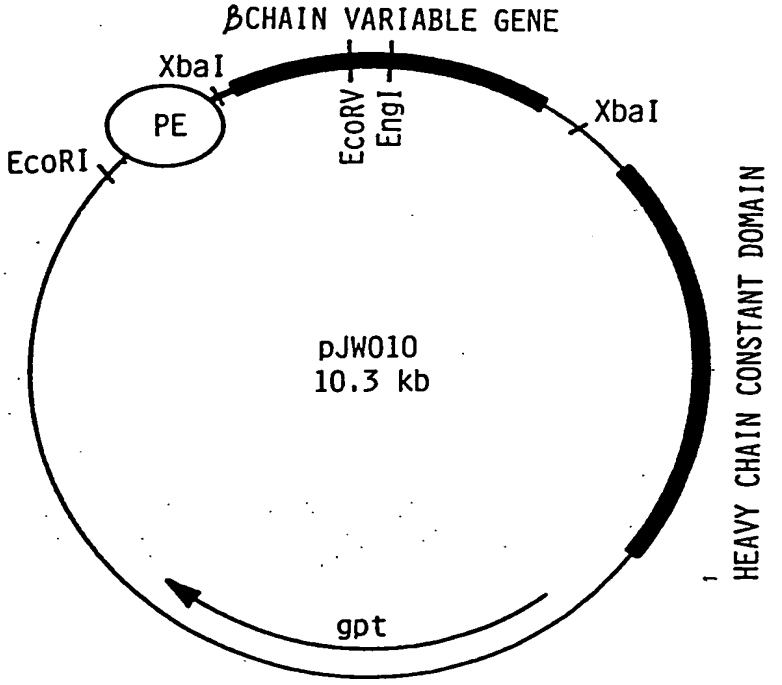


FIG. 16B

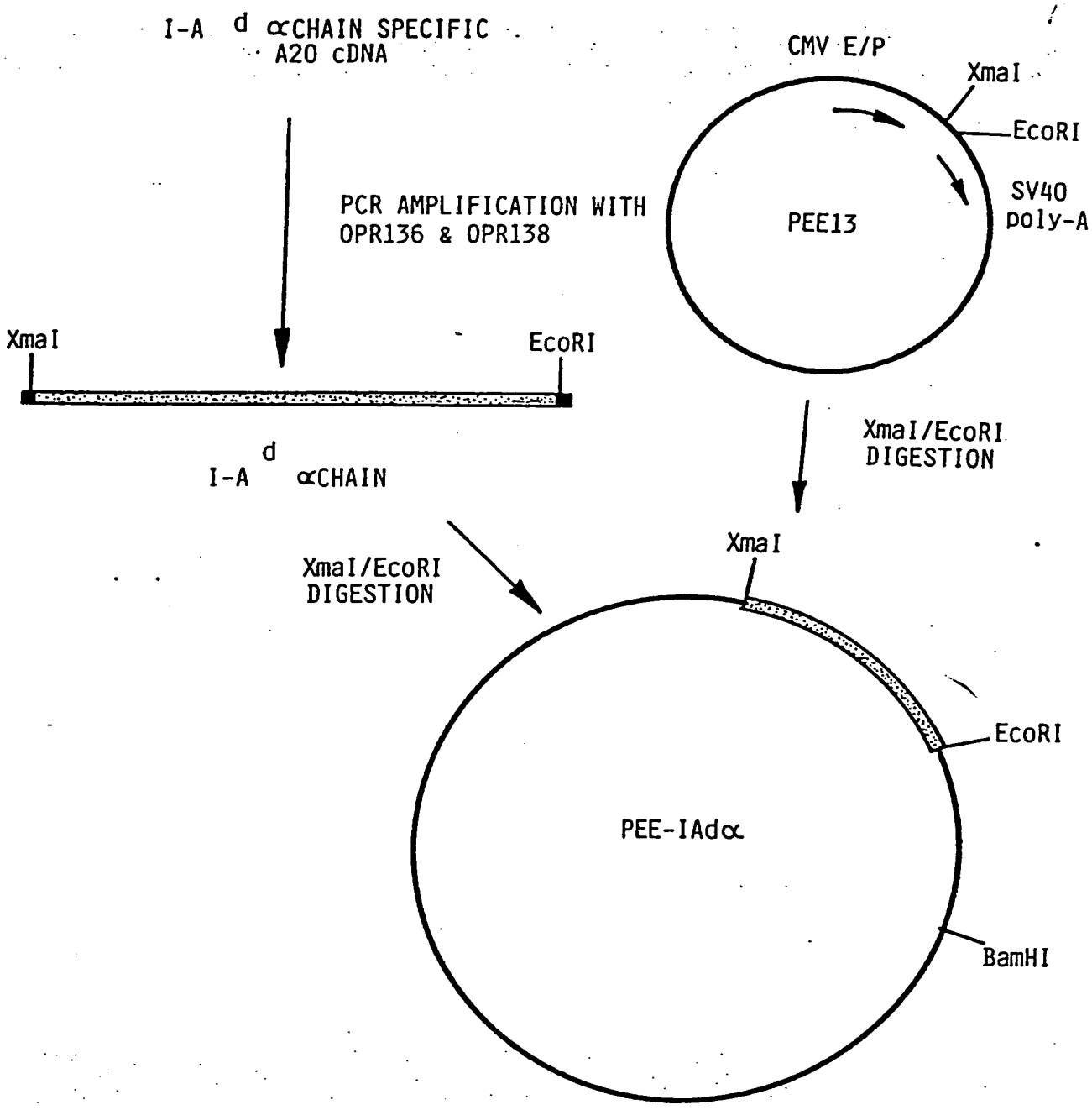


FIG. 17A

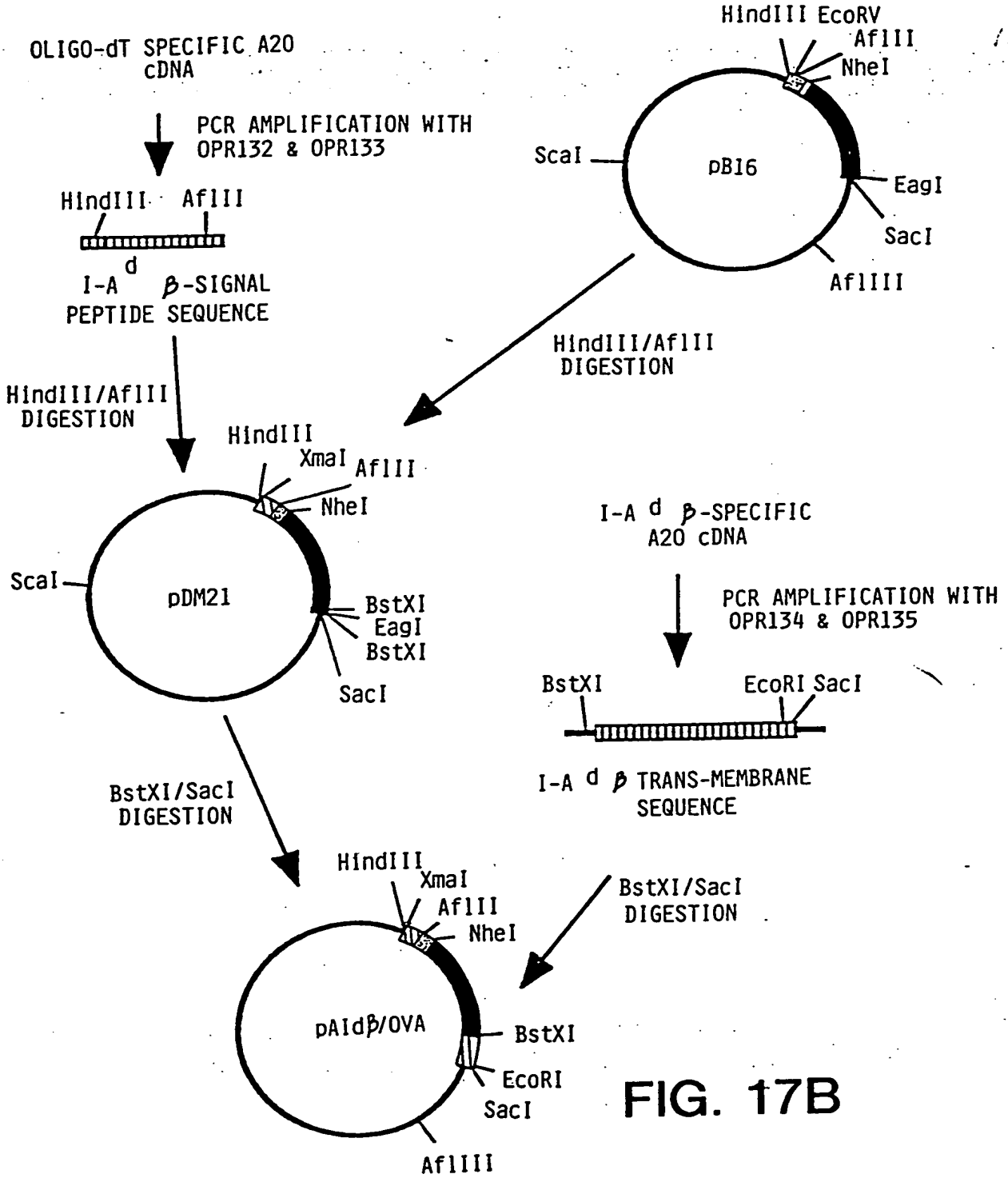

OLIGO-dT SPECIFIC A20 cDNA
PCR AMPLIFICATION WITH OPR132 & OPR133
HindIII AflII
I-A d β-SIGNAL PEPTIDE SEQUENCE
HindIII/AflII DIGESTION
HindIII EcoRV AflII NheI
ScaI
pB16
EagI
SacI
AflIII
HindIII/AflII DIGESTION
HindIII XmaI AflII NheI
ScaI
pDM21
BstXI EagI BstXI
SacI
I-A d β-SPECIFIC A20 cDNA
PCR AMPLIFICATION WITH OPR134 & OPR135
BstXI EcoRI SacI
I-A d β TRANS-MEMBRANE SEQUENCE
BstXI/SacI DIGESTION
HindIII XmaI AflII NheI
BstXI/SacI DIGESTION
pAIdβ/OVA
BstXI
EcoRI
SacI
AflIII

FIG. 17B

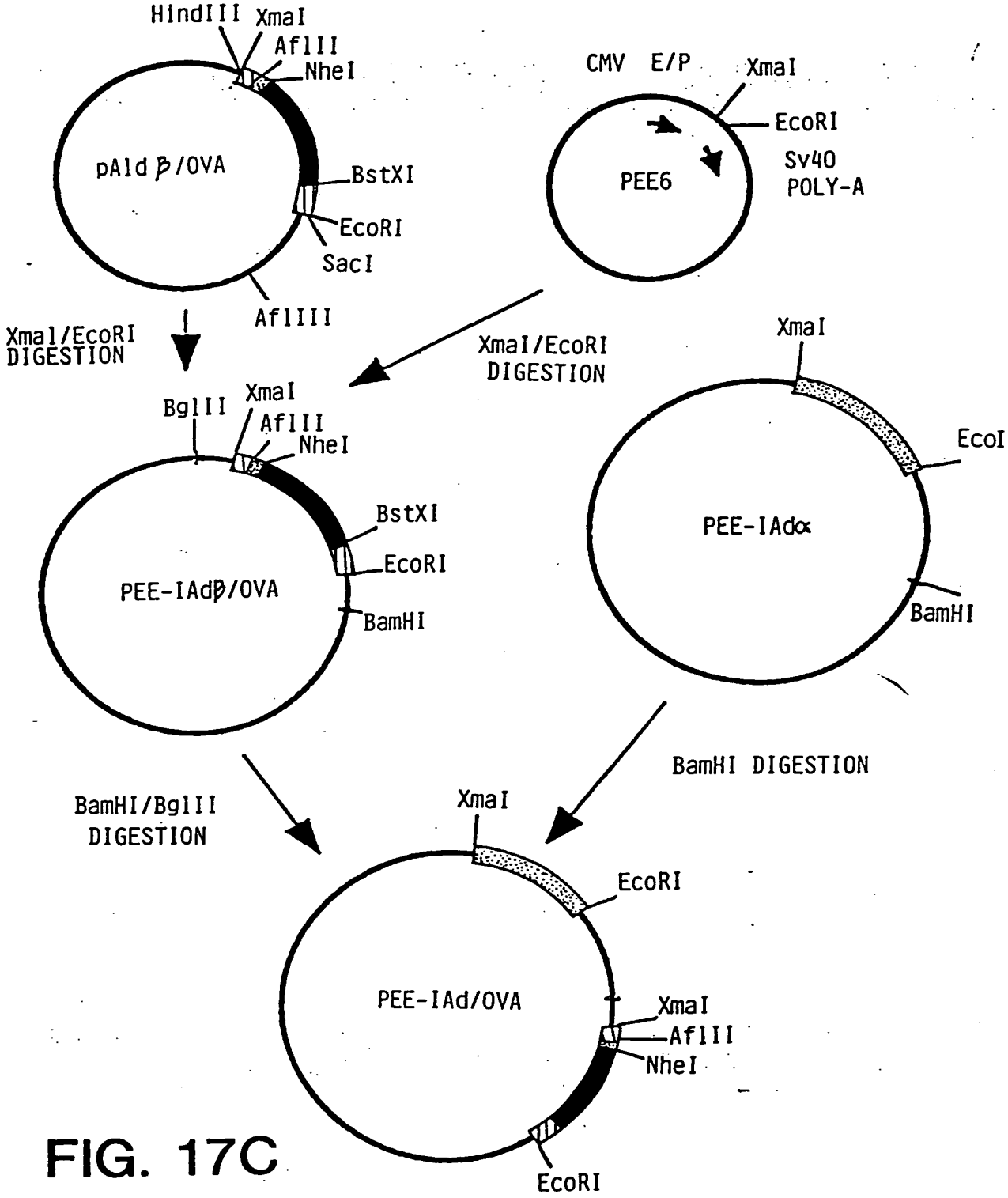

HindIII
XmaI
AflII
NheI
pAldβ/OVA
BstXI
EcoRI
SacI
AflIII
CMV E/P
XmaI
EcoRI
PEE6
Sv40
POLY-A
XmaI/EcoRI
DIGESTION
XmaI/EcoRI
DIGESTION
XmaI
BglII
XmaI
AflII
NheI
BstXI
EcoRI
PEE-IAdβ/OVA
BamHI
XmaI
EcoI
PEE-IAdα
BamHI
BamHI DIGESTION
BamHI/BglII
DIGESTION
XmaI
EcoRI
PEE-IAd/OVA
XmaI
AflII
NheI
EcoRI

FIG. 17C

```
XbaI
           10             20              30                40              50
CCCGGGCCAC C ATG CCG TGC AGC AGA GCT CTG ATT CTG GGG GTC CTC GCC
GGGCCCGGTG G TAC GGC ACG TCG TCT CGA GAC TAA GAC CCC CAG GAG CGG
              M   P   C   S   R   A   L   I   L   G   V   L   A
             I-Ad α CHAIN SIGNAL PEPTIDE
       KOZAK
     CONSENSUS

            60          70              80              90
CTG AAC ACC ATG CTC AGC CTC TGC GGA GGT GAA GAC GAC ATT GAG //
GAC TTG TGG TAC GAG TCG GAG ACG CCT CCA CTT CTG CTG TAA CTC //
 L   N   T   M   L   S   L   C   G   G ↑ E   D   D   I   E  //
                                         +1
I-Ad α CHAIN SIGNAL PEPTIDE   SIGNAL PEPTIDE
                              CLEAVAGE SITE
                                                     EcoRI
        750         760             770         780
CGA TCA GGT GGC ACC TCC AGA CAC CCA GGG CCT TTA TGA GAATTC
GCT AGT CCA CCG TGG AGG TCT GTG GGT CCC GGA AAT ACT CTTAAG
 R   S   G   G   T   S   R   H   P   G   P   L   *
                                                STOP
      I-Ad α CHAIN
```

FIG. 18A

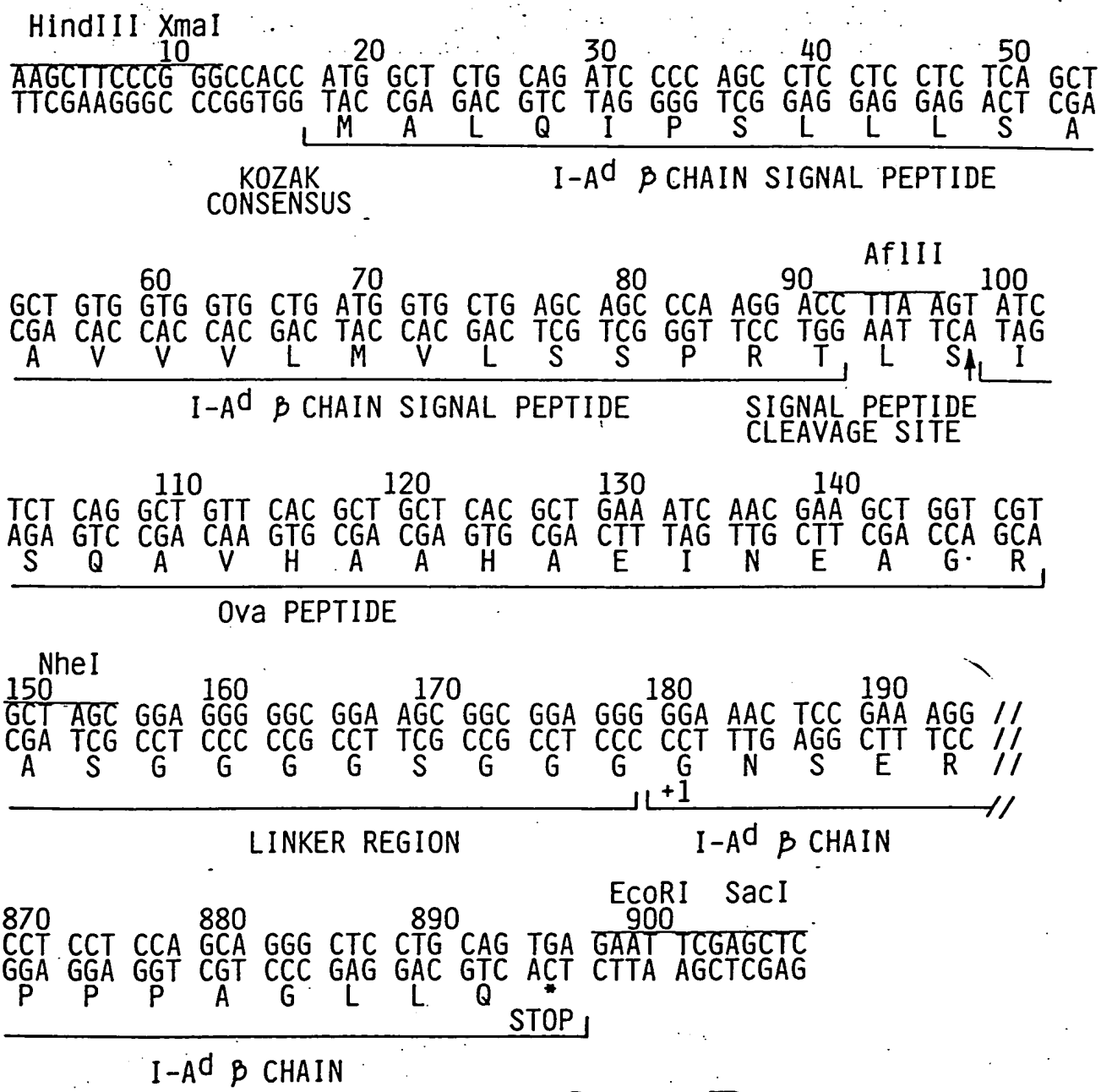


FIG. 18B

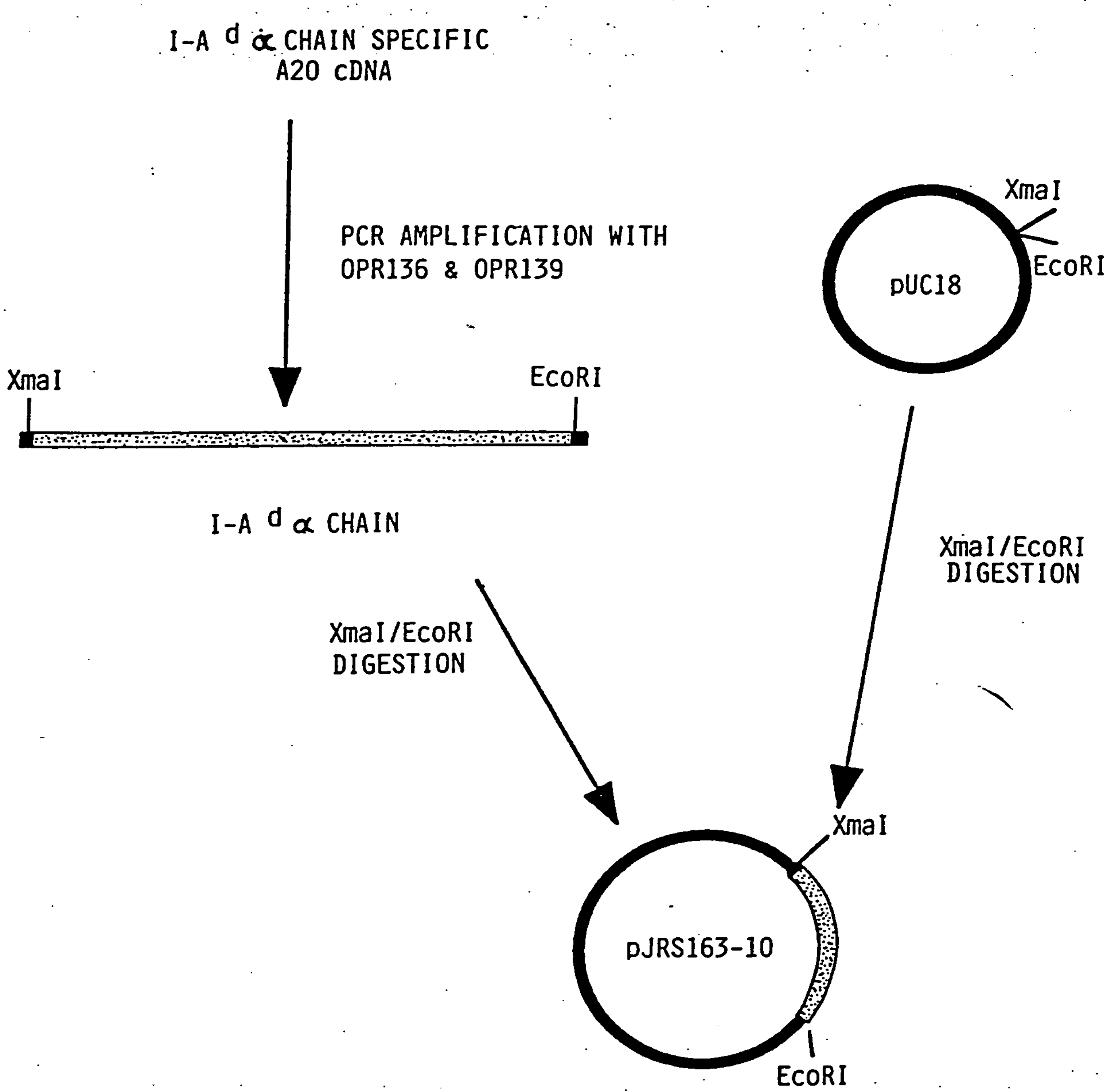


FIG. 19A

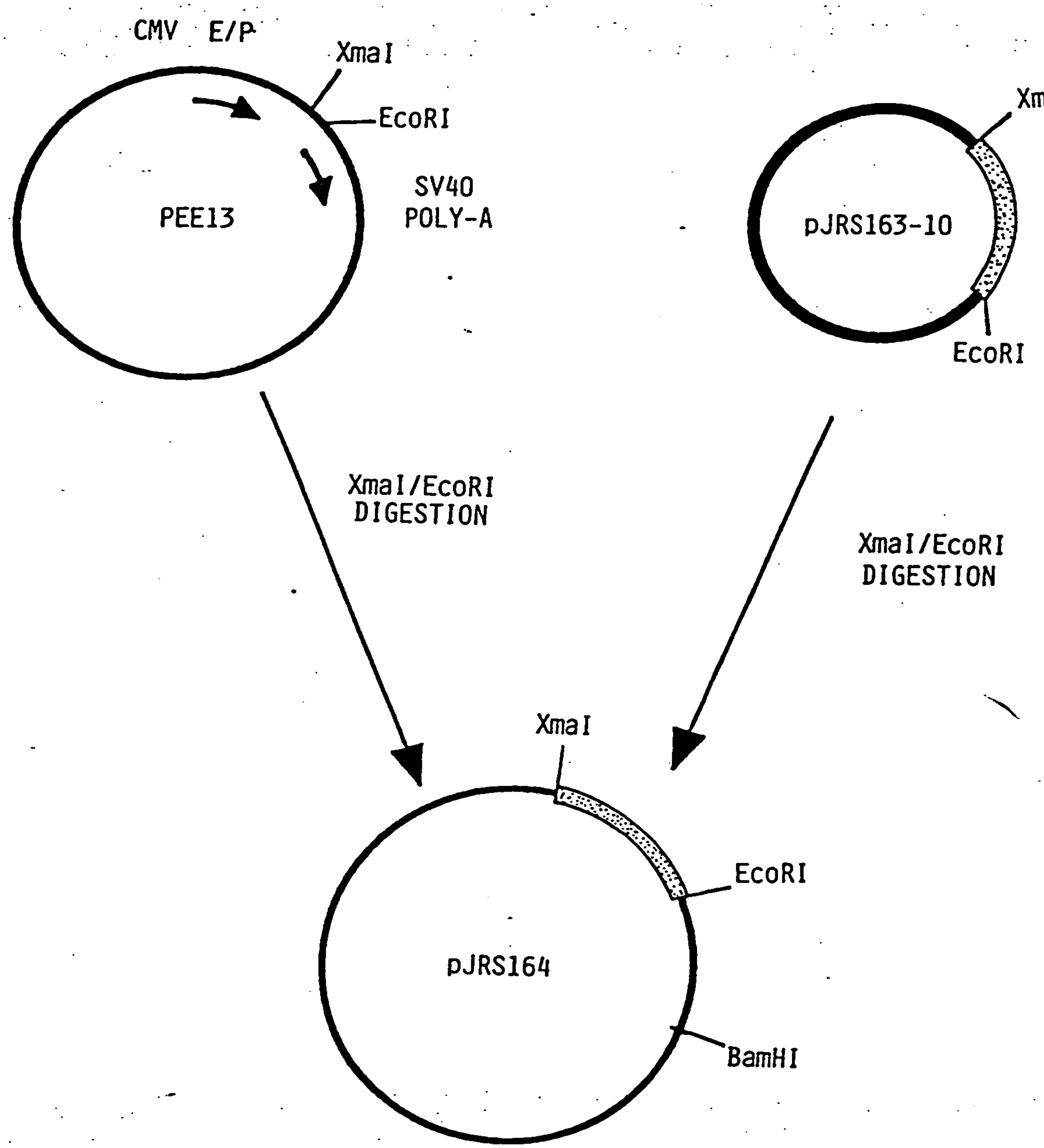

CMV E/P
XmaI
EcoRI
PEE13
SV40
POLY-A
XmaI
pJRS163-10
EcoRI
XmaI/EcoRI
DIGESTION
XmaI/EcoRI
DIGESTION
XmaI
EcoRI
pJRS164
BamHI

FIG. 19B

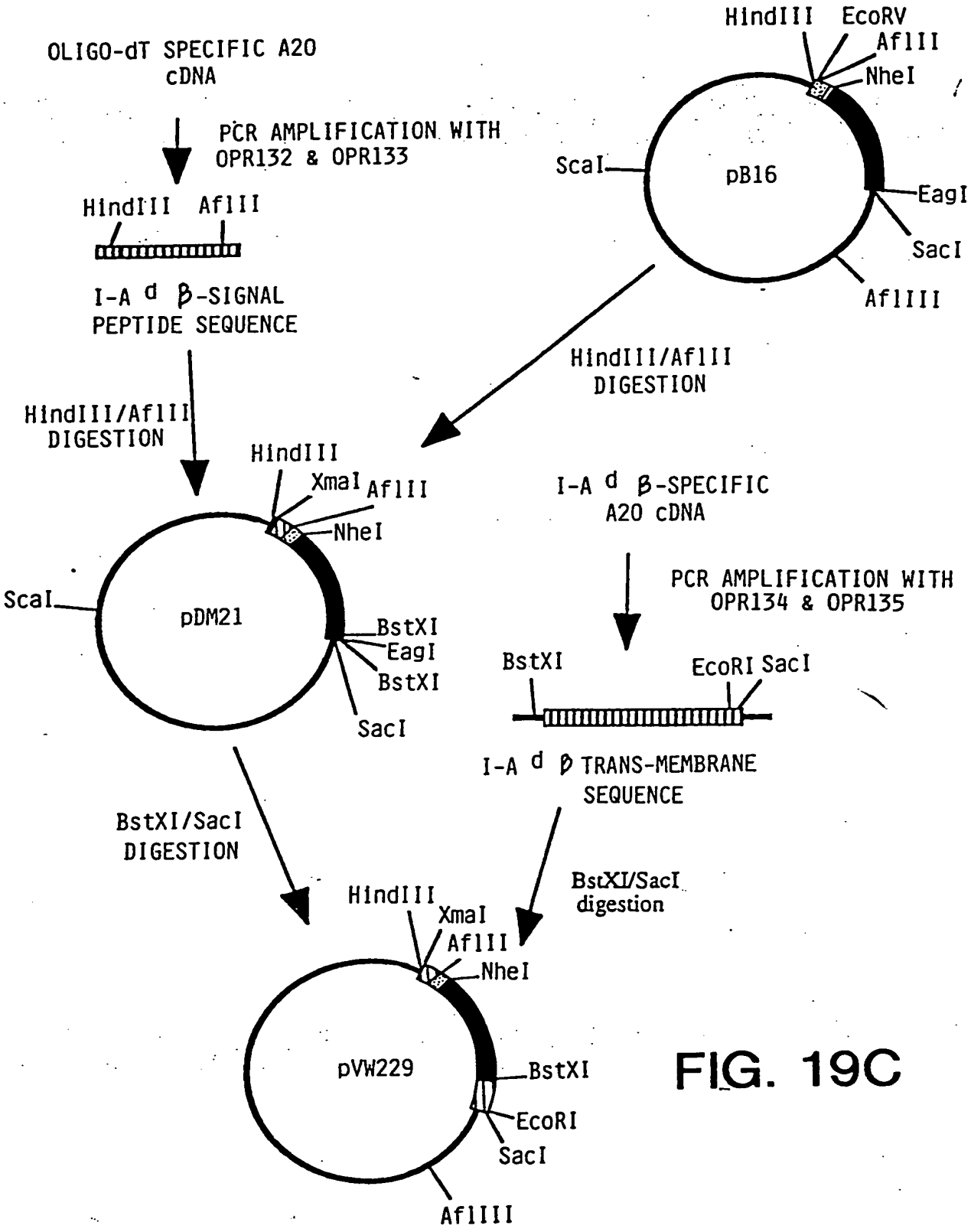


FIG. 19C

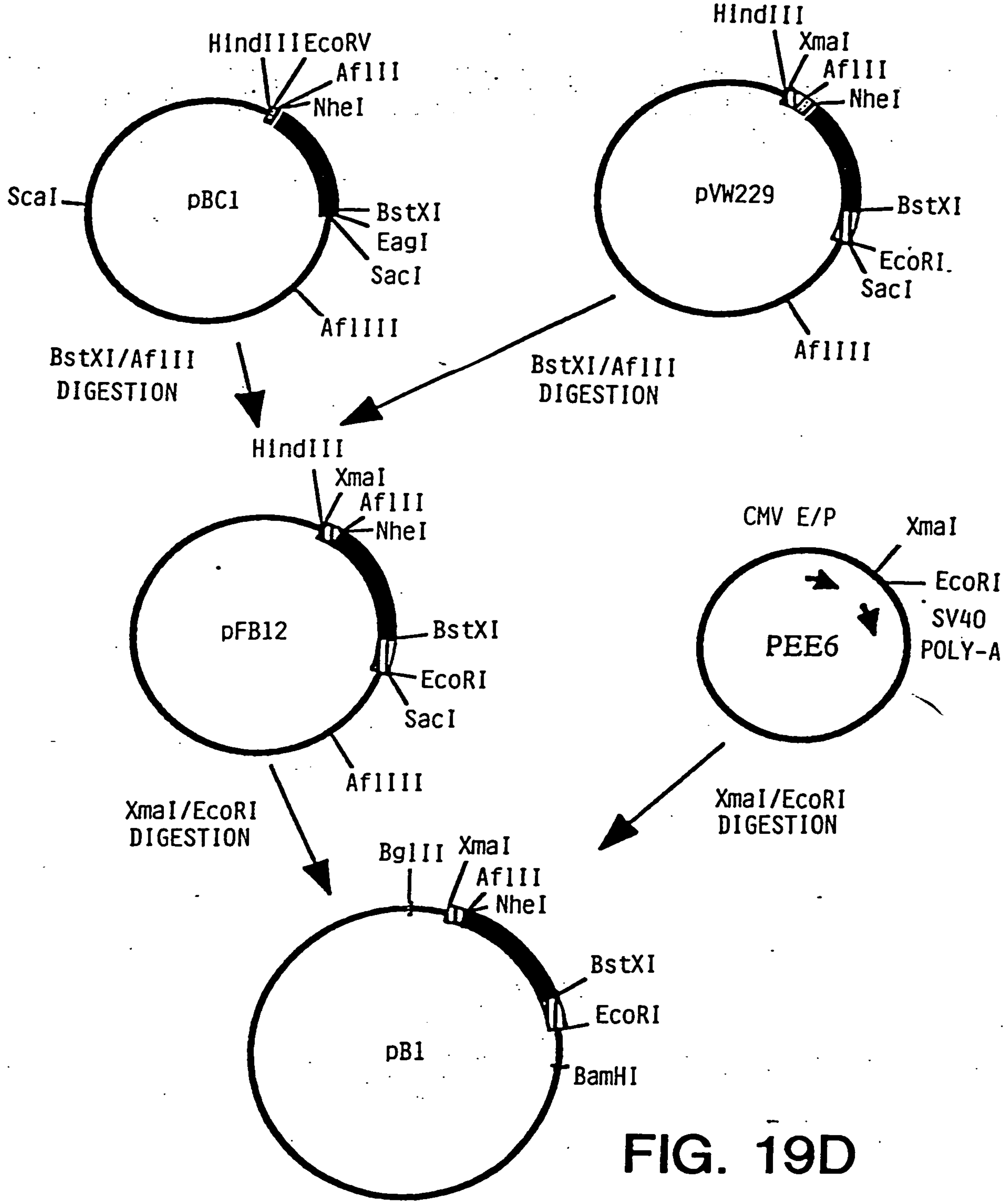


FIG. 19D

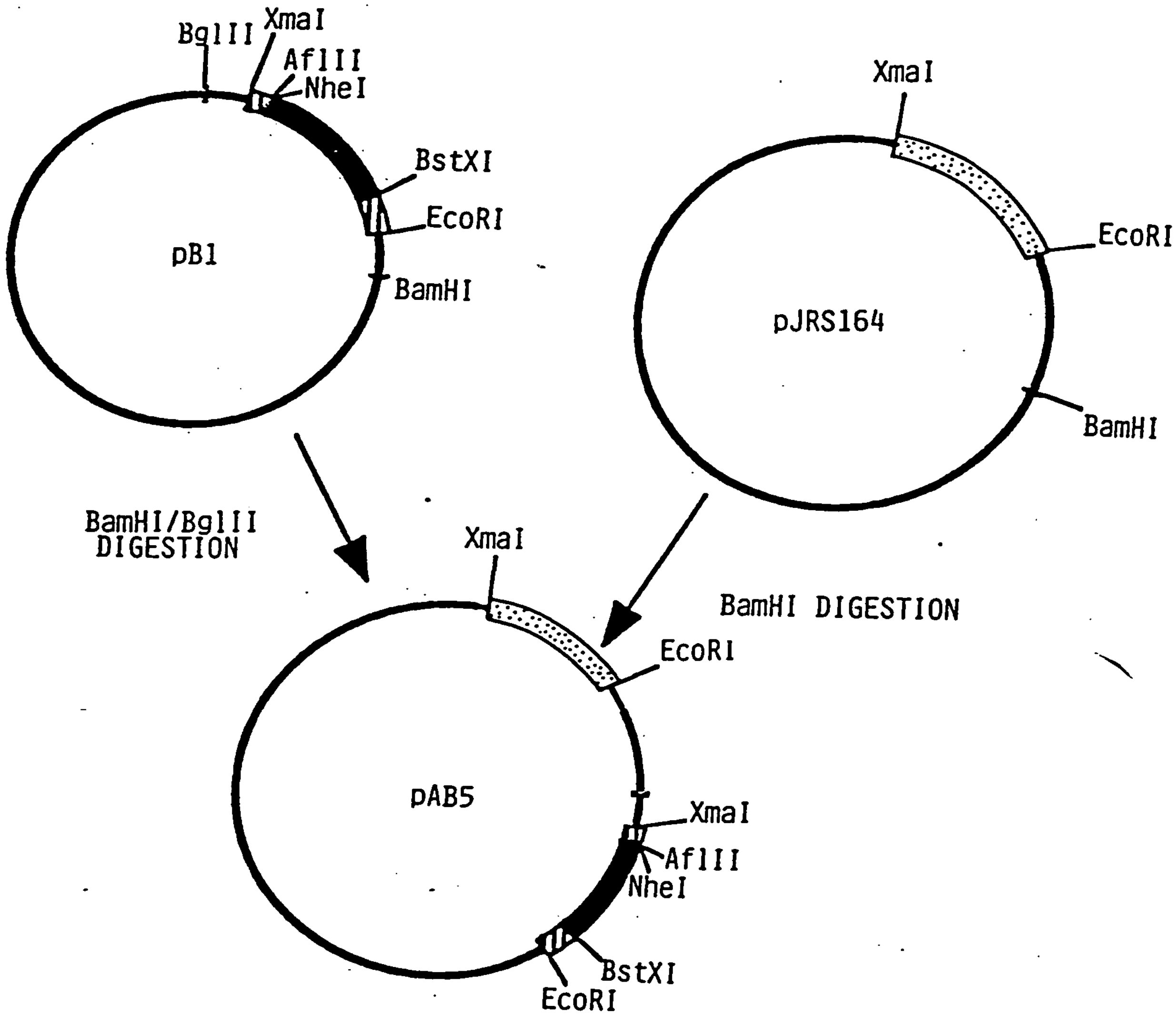


FIG. 19E

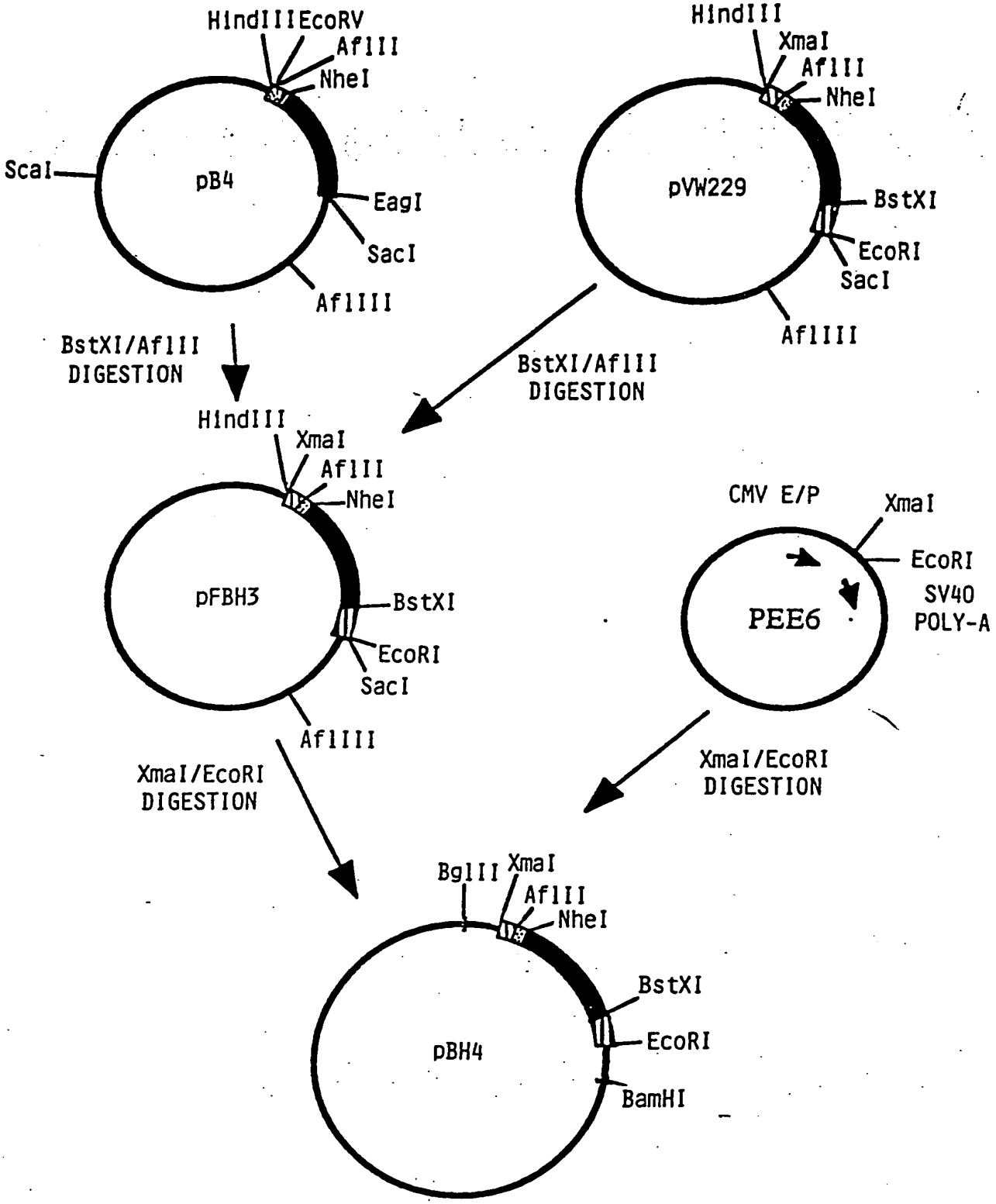

HindIII EcoRV
AflII
NheI
ScaI
pB4
EagI
SacI
AflIII
HindIII
XmaI
AflII
NheI
pVW229
BstXI
EcoRI
SacI
AflIII
BstXI/AflII
DIGESTION
BstXI/AflII
DIGESTION
HindIII
XmaI
AflII
NheI
pFBH3
BstXI
EcoRI
SacI
AflIII
CMV E/P
XmaI
EcoRI
SV40
POLY-A
PEE6
XmaI/EcoRI
DIGESTION
XmaI/EcoRI
DIGESTION
BglII
XmaI
AflII
NheI
BstXI
EcoRI
BamHI
pBH4

FIG. 19F

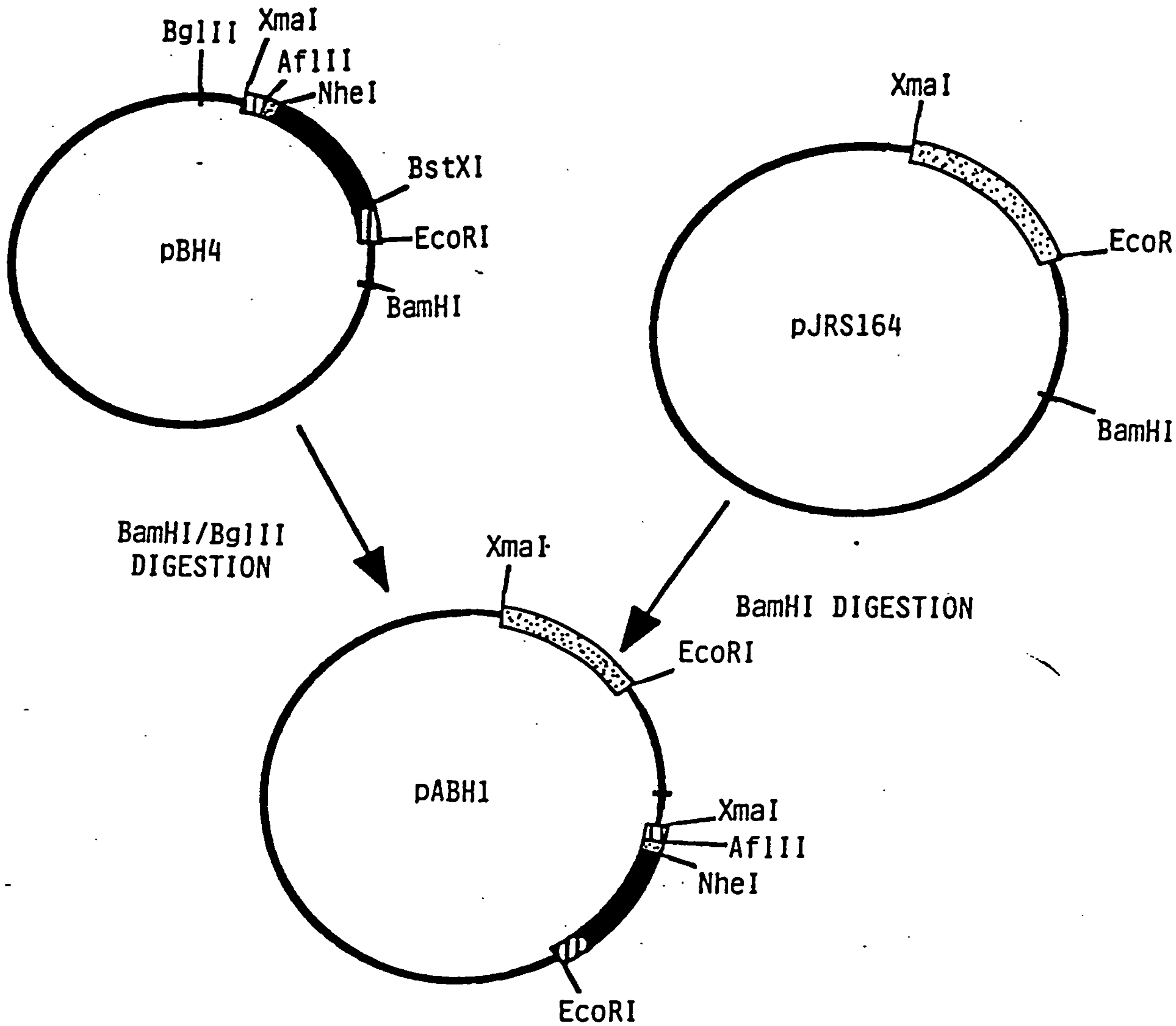


FIG. 19G

OPR132
I-A^d β signal peptide front primer with Kozak consensus for CellTech vector - HindIII/XmaI sites
5′-CCC CCC AAG CTT CCC GGG CCA CCA TGG CTC TGC AGA TCC CCA GC-3′

OPR133
I-A^d β signal peptide back primer with Kozak consensus for CellTech vector - AflII site
5′-CCC CCC ACT TAA GGT CCT TGG·GCT GCT CAG CAC C-3′

OPR134
I-A^d β transmembrane front primer for CellTech vector - BstXI sites
5′-CCC CCC CCA TCA CTG TGG AGT GGA GGG-3′

OPR135
I-A^d β transmembrane back primer for CellTech vector - SstI, EcoRI sites
5′-CCC CCC GAG CTC GAA TCC TCA CTG CAG GAG CCC TGC TGG-3′

OPR136
I-A^d α signal peptide front primer with Kozak consensus for CellTech vector - HindIII/XmaI sites
5′-CCC CCC AAG CTT CCC GGG CCA CCA TGC CGT GCA GCA GAG CTC TG-3′

OPR139
I-A^d α transmembrane primer for CellTech vector - SstI/EcoRI sites
5′-CCC CCC GAG CTC GAA TCC TCA TAA AGG CCC TGG GTG TCT G-3′

B7-1-2F
Murine B7-1 front primer with Kozak consensus for CloneTech vector - NotI site
5′-CCC CCC CCG CGG CCG CCC CAC CAT GGG ACT GAG TAA CAT TCT C-3′

B7-1-2B
Murine B7-1 BACK primer for CloneTech vector - NotI site
5′-CCC CCC GCG GCC GCT TTA AAA ACA TGT ATC ACT TTT-3′

FIG. 20

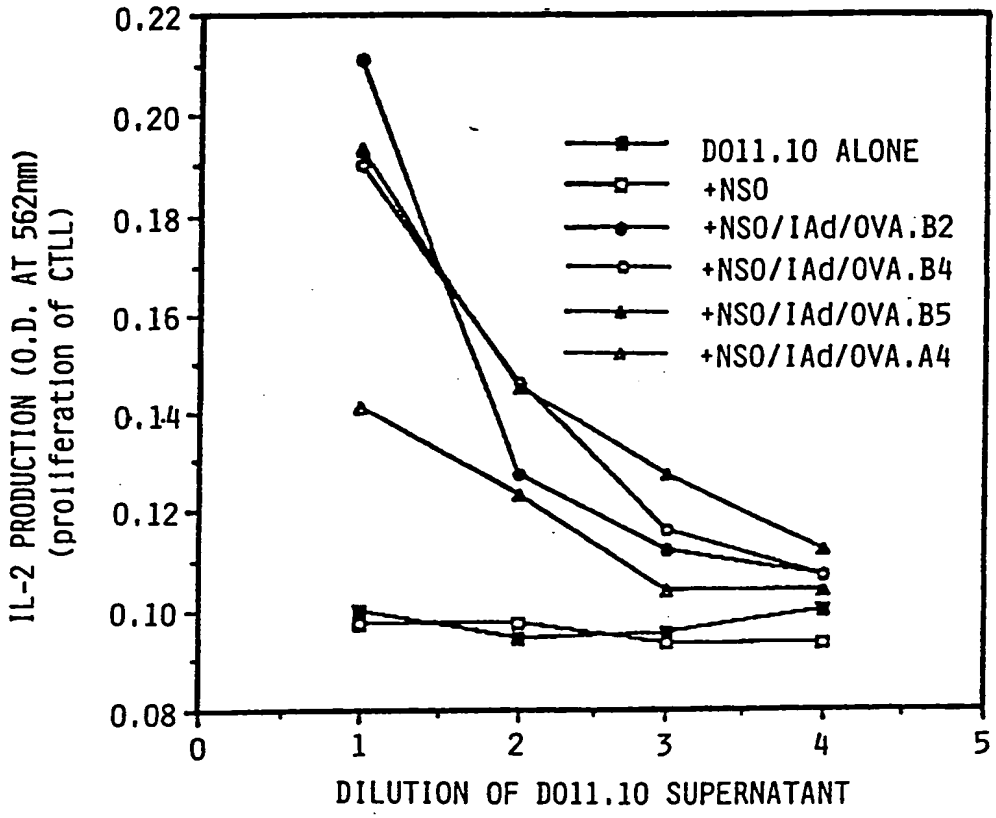


FIG. 21

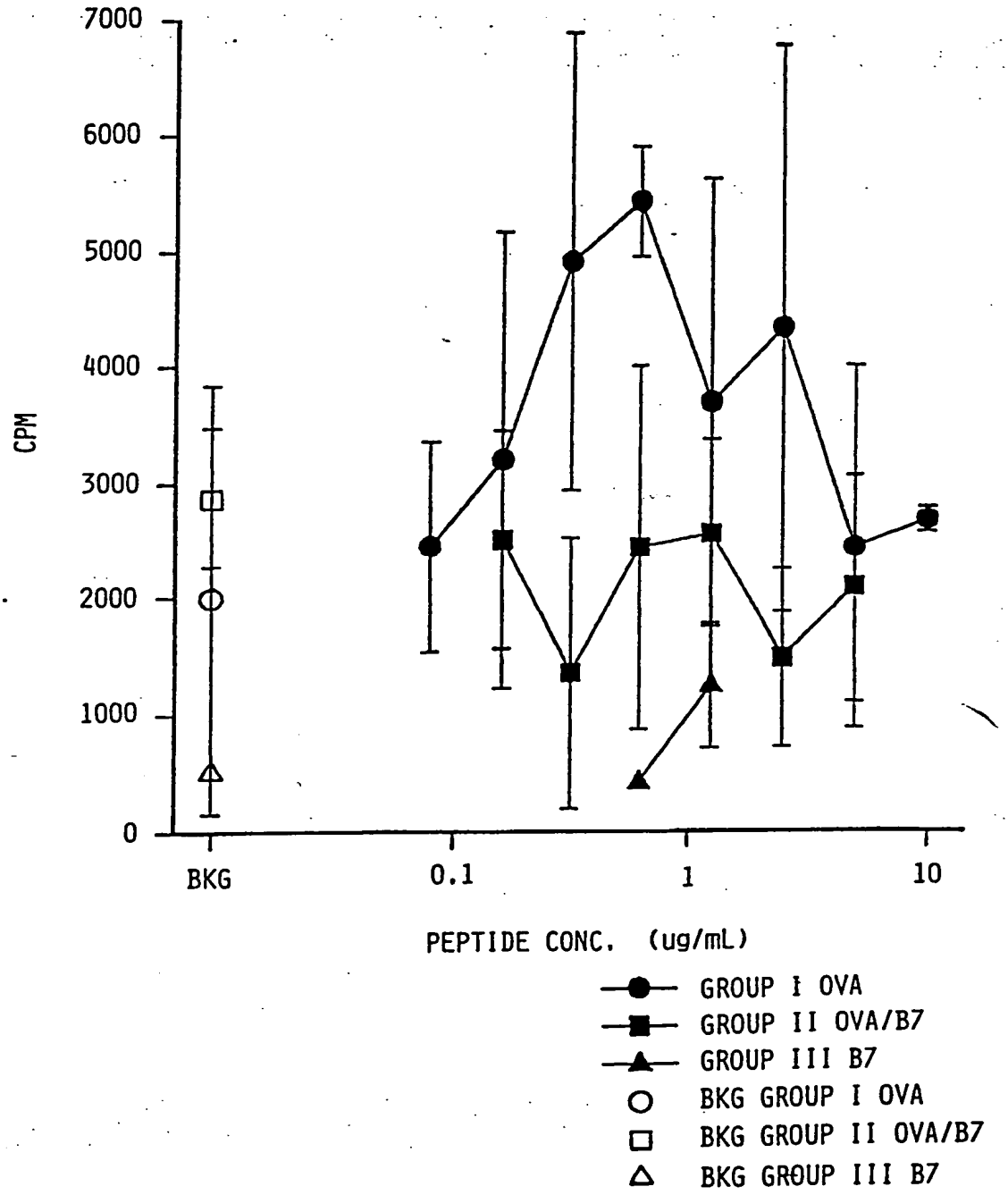

7000
6000
5000
4000
3000
2000
1000
0
CPM
BKG
0.1
1
10
PEPTIDE CONC. (ug/mL)
GROUP I OVA
GROUP II OVA/B7
GROUP III B7
BKG GROUP I OVA
BKG GROUP II OVA/B7
BKG GROUP III B7

FIG. 22

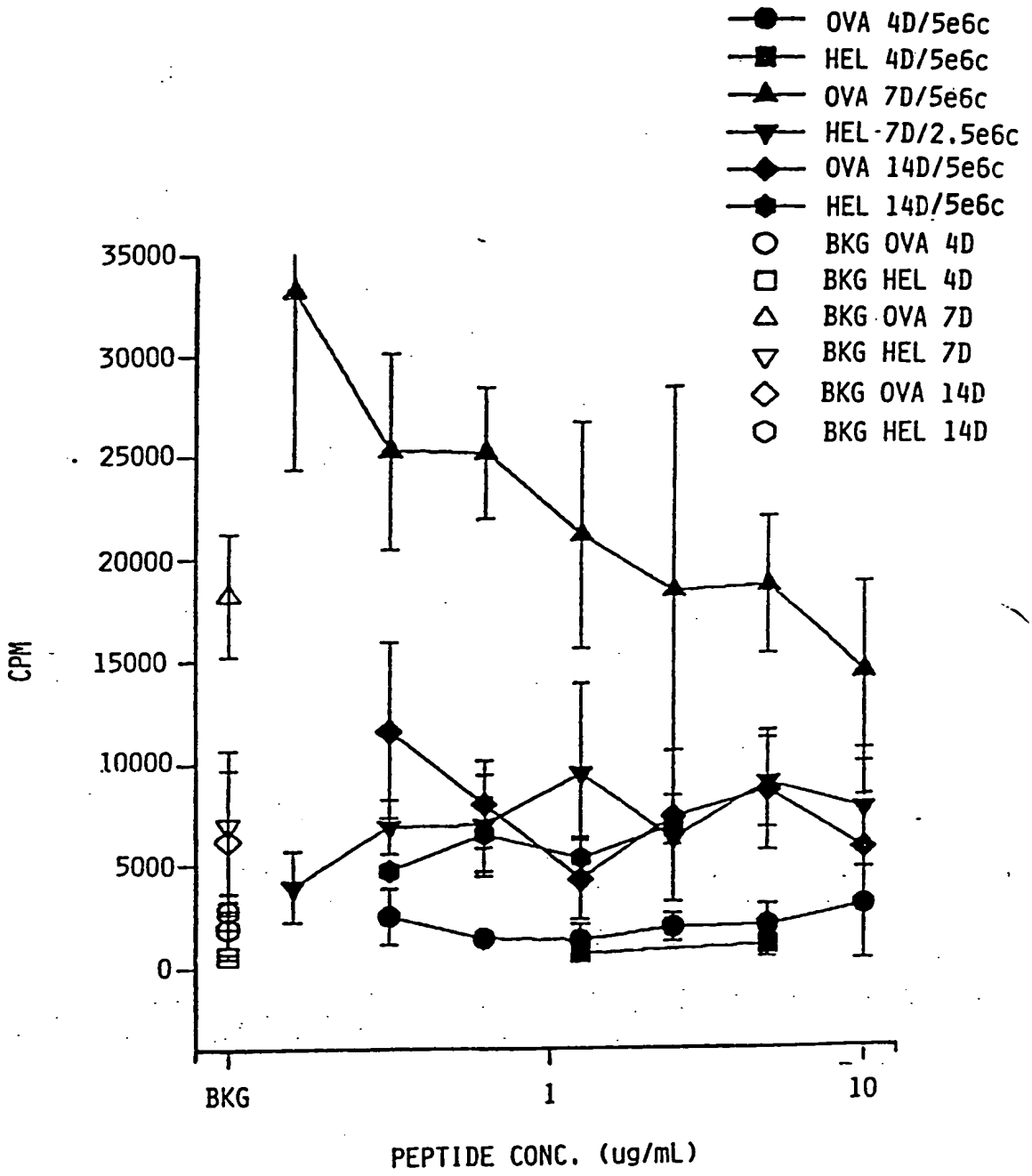

OVA 4D/5e6c
HEL 4D/5e6c
OVA 7D/5e6c
HEL 7D/2.5e6c
OVA 14D/5e6c
HEL 14D/5e6c
BKG OVA 4D
BKG HEL 4D
BKG OVA 7D
BKG HEL 7D
BKG OVA 14D
BKG HEL 14D
35000
30000
25000
20000
15000
10000
5000
0
CPM
BKG
1
10
PEPTIDE CONC. (ug/mL)

FIG. 23

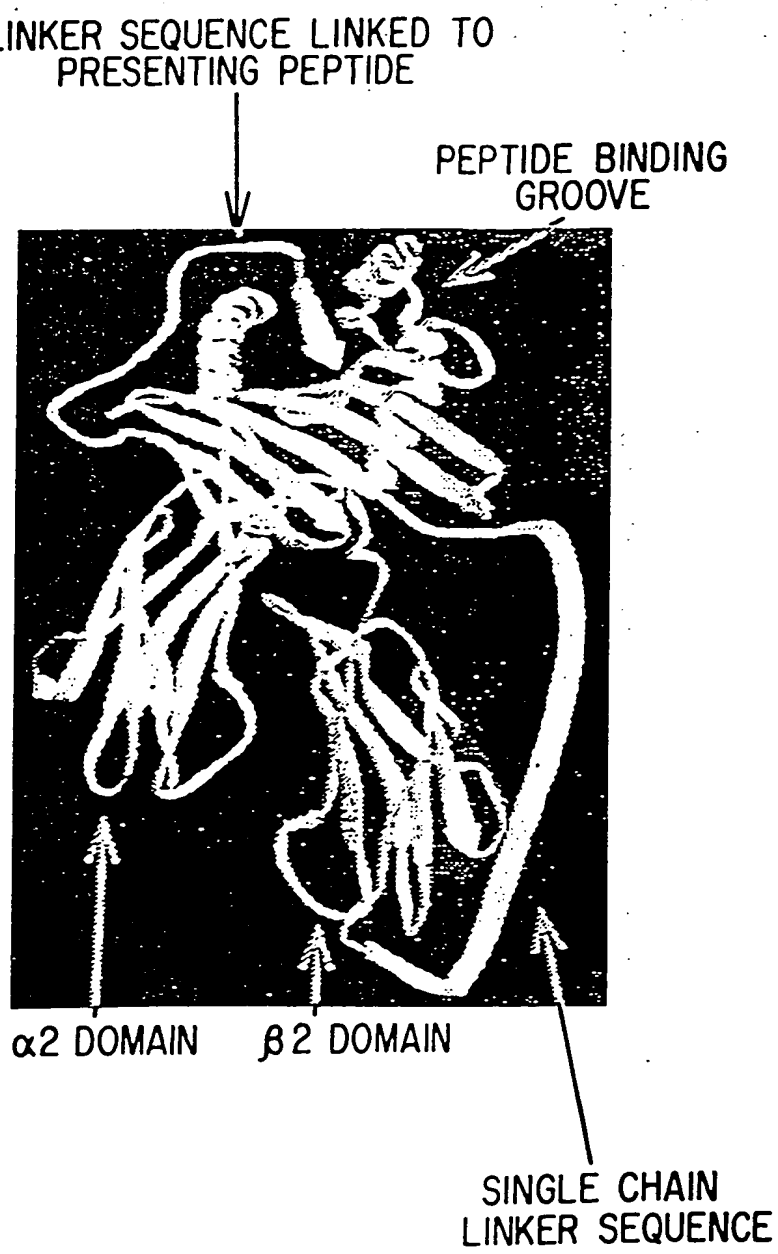


FIG. 24

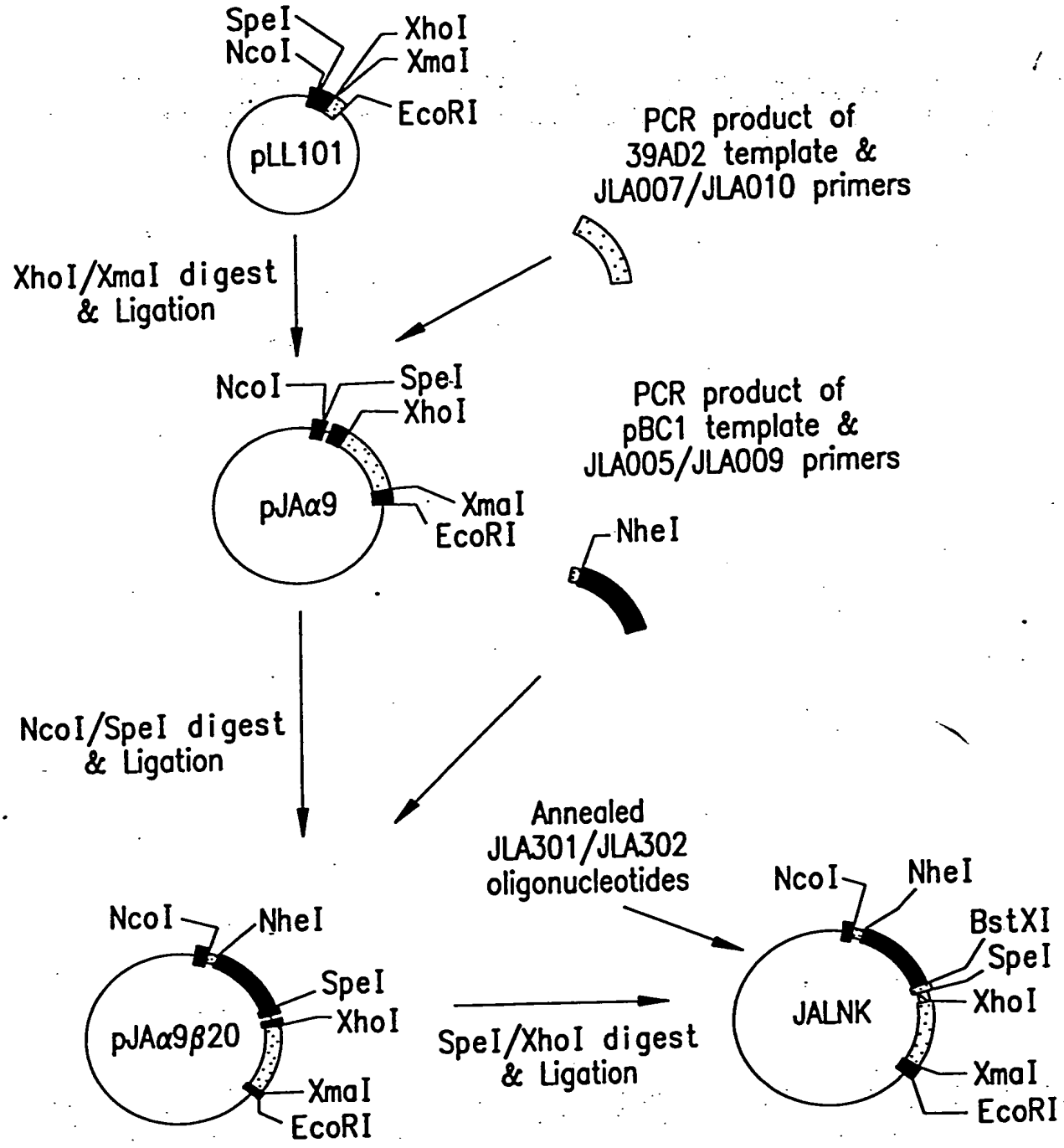


FIG.25A

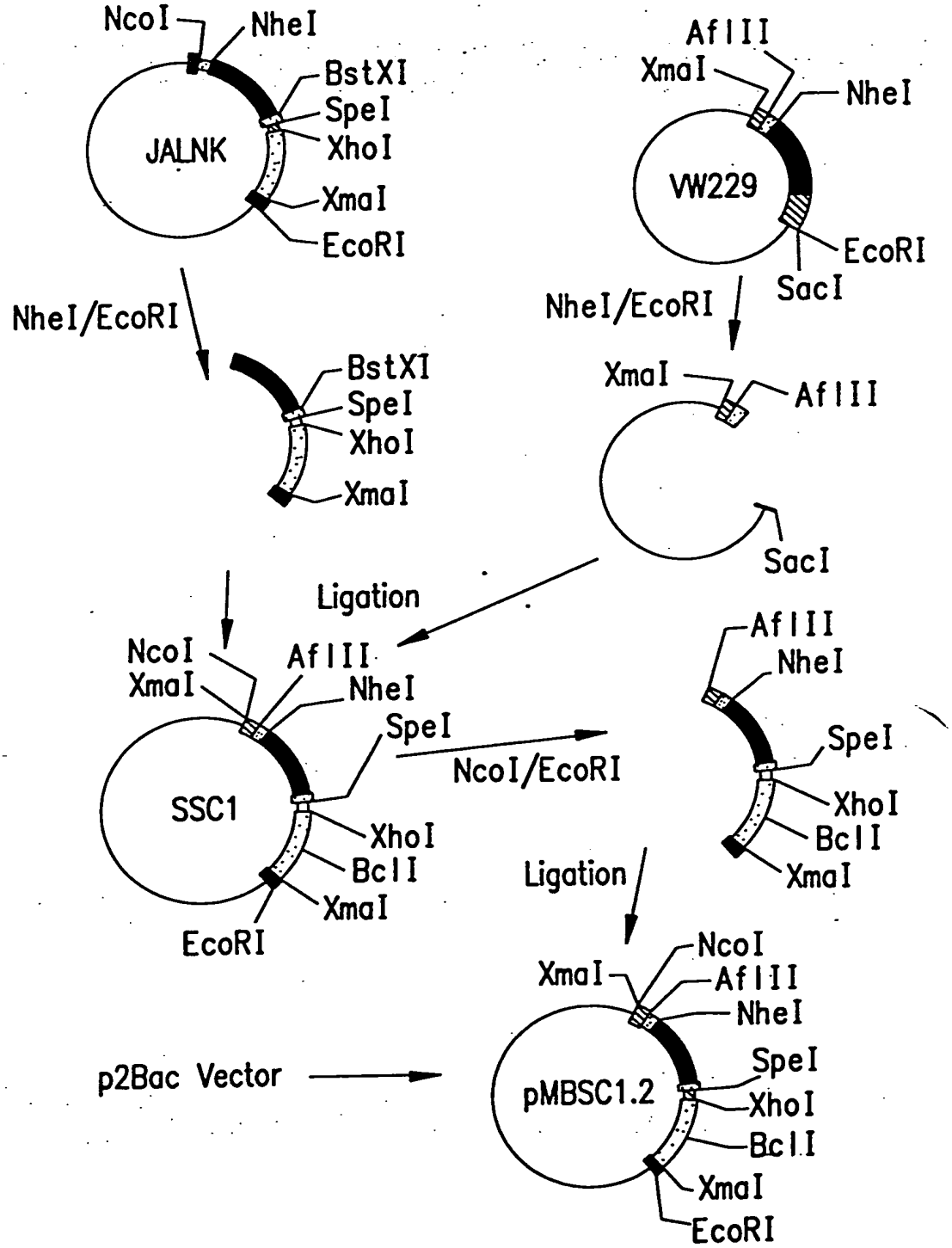

NcoI
NheI
BstXI
SpeI
XhoI
XmaI
EcoRI
JALNK
NheI/EcoRI
AflII
XmaI
NheI
VW229
EcoRI
SacI
NheI/EcoRI
XmaI
AflII
SacI
Ligation
NcoI
XmaI
AflII
NheI
SpeI
SSC1
XhoI
BclI
XmaI
EcoRI
NcoI/EcoRI
AflII
NheI
SpeI
XhoI
BclI
XmaI
Ligation
p2Bac Vector
NcoI
XmaI
AflII
NheI
SpeI
pMBSC1.2
XhoI
BclI
XmaI
EcoRI

FIG.25B

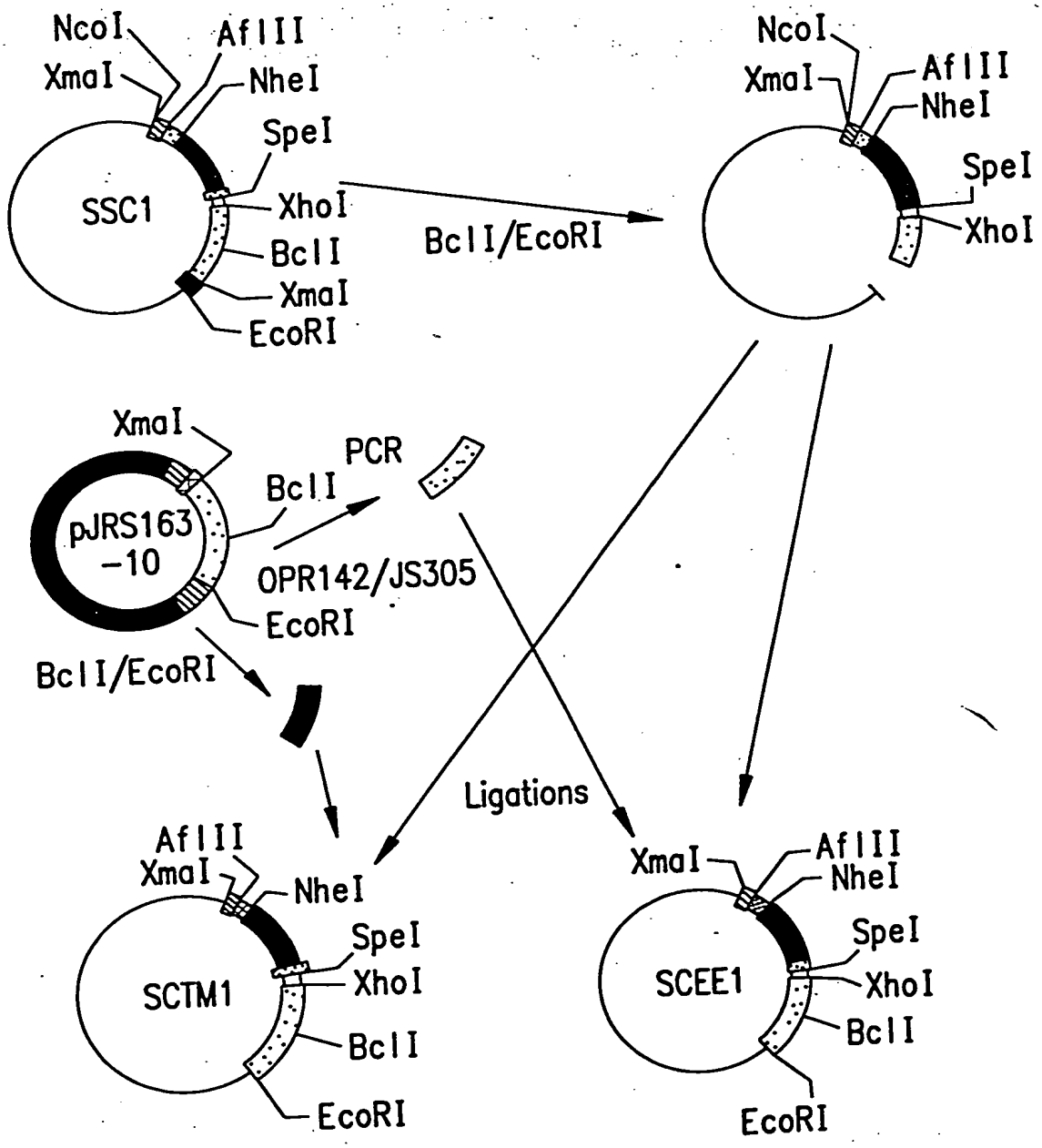

NcoI
AflII
XmaI
NheI
SpeI
SSC1
XhoI
BclI
XmaI
EcoRI
BclI/EcoRI
NcoI
XmaI
AflII
NheI
SpeI
XhoI
XmaI
PCR
BclI
pJRS163
-10
OPR142/JS305
EcoRI
BclI/EcoRI
Ligations
AflII
XmaI
NheI
SpeI
SCTM1
XhoI
BclI
EcoRI
XmaI
AflII
NheI
SpeI
SCEE1
XhoI
BclI
EcoRI

FIG.25C

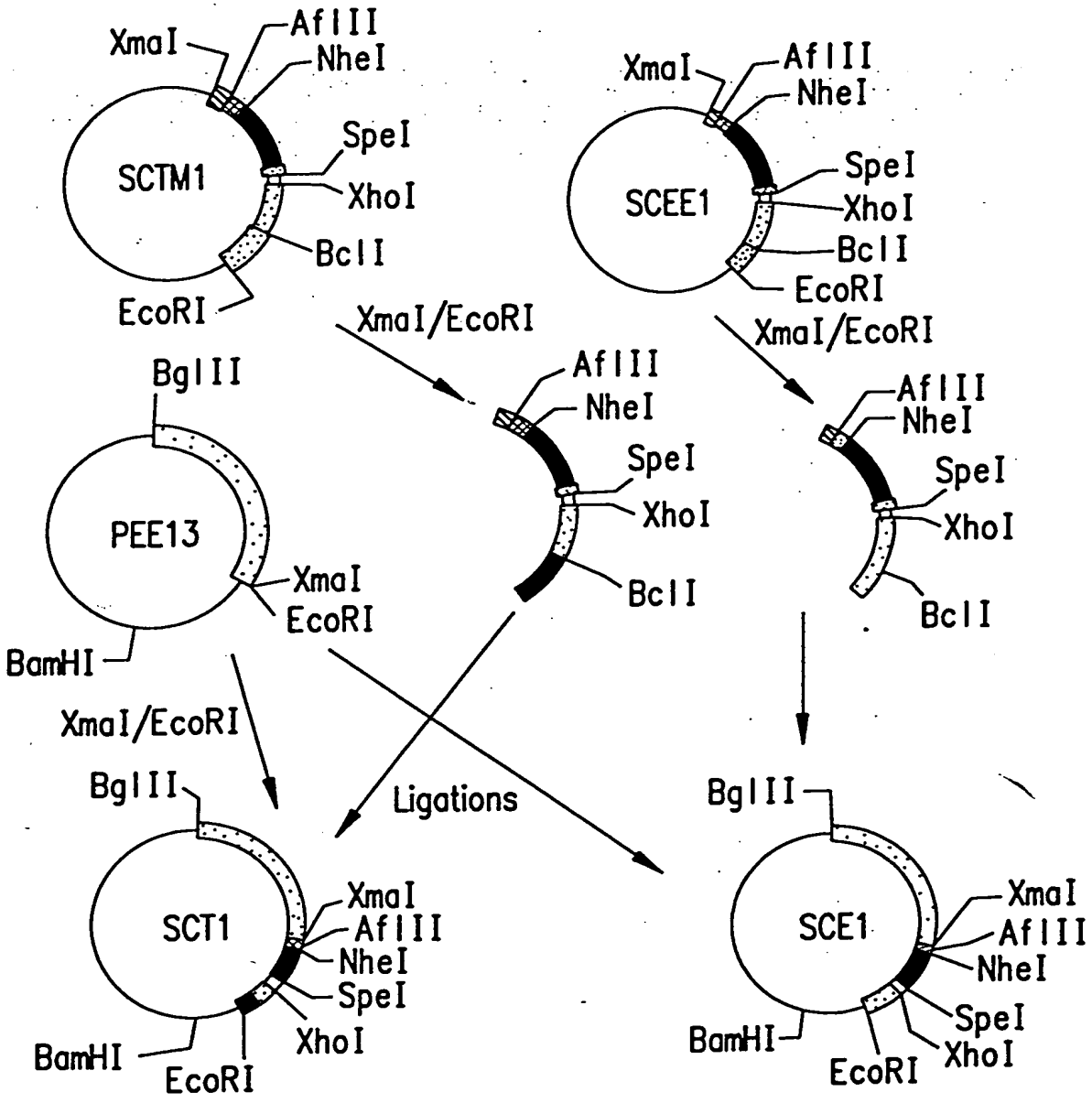

XmaI
AflII
NheI
SpeI
XhoI
BclI
EcoRI
SCTM1
SCEE1
XmaI/EcoRI
BglII
PEE13
BamHI
Ligations
SCT1
SCE1

FIG.25D

JLA-005
5'-CCCCCCGCCATGGCCGCTAGCGGAGGGGGCGGAAGC-3'

JLA-007
5'-CCCGGGGCCTCGAGTGAAGACGACATTGAGGCCGAC-3'

JLA-009
5'-CCCCCCACTAGTCCACTCCACAGTGATGGGGCT-3'

JLA-010
5'-CCCCCCCCCGGGACCAGTGTTTCAGAACCGGCTCCTC-3'

JLA-301
5'-TCGAGGAACCGCCACCGCCAGAACCGCCGCCACCGGA-
ACCACCACCGCCGCTGCCACCGCCACCA-3'

JLA-302
5'-CTAGTGGTGGCGGTGGCAGCGGCGGTGGTGGTTCCGG-
TGGCGGCGGTTCTGGCGGTGGCGGTTCC-3'

OPR-142
5'-CTTGGGAATCTTGACTAAGAGG-3'

JS-305
5'-CAGGTCGAATTCTCATTCCATCGGCATGTACTCTTCTT-
CCTCCCAGTGTTTCAGAACCGG-3'

FIG.26

```
          10          20          30          40          50
           *           *           *           *           *
CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG
GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC
      M   A   L   Q   I   P   S   L   L   L   S   A   A   V   V>
     <---------------- I-Ad β-CHAIN LEADER ----------------------

          60          70          80          90
           *           *           *           *
GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
 V   L   M   V   L   S   S   P   R   T   L   S   I   S   Q   A>
-------------------------------------------------------------

100         110         120         130         140
 *           *           *           *           *
GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT
 V   H   A   A   H   A   E   I   N   E   A   G   R   A   S   G>
------  OVA 323-339  ----------------------------><----------

  150         160         170         180         190
   *           *           *           *           *
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
 G   G   G   S   G   G   G   G   N   S   E   R   H   F   V   V>

-- 10  AMINO ACID LINKER--><-------  I-Ad β-1 DOMAIN  ---------

    200         210         220         230         240
     *           *           *           *           *
CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC
 Q   F   K   G   E   C   Y   Y   T   N   G   T   Q   R   I   R>
-------------------------------------------------------------

       250         260         270         280         290
        *           *           *           *           *
CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG
 L   V   T   R   Y   I   Y   N   R   E   E   Y   V   R   Y   D>
-------------------------------------------------------------
```

FIG.27A

```
       300        310        320        330
        *          *          *          *
AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG
 S   D   V   G   E   Y   R   A   V   T   E   L   G   R   P   D>
----------------------------------------------------------------

340        350        360        370        380
 *          *          *          *          *
GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC
CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG
 A   E   Y   W   N   S   Q   P   E   I   L   E   R   T   R   A>
----------------------------------------------------------------

   390        400        410        420        430
    *          *          *          *          *
GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC
CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG
 E   V   D   T   A   C   R   H   N   Y   E   G   P   E   T   S>
----------------------------------------------------------------

      440        450        460        470        480
       *          *          *          *          *
ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC
TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG
 T   S   L   R   R   L   E   Q   P   N   V   A   I   S   L   S>
--- I-Ad β-1 DOMAIN ->&lt;------- I-Ad β-2 DOMAIN -------------

         490        500        510        520        530
          *          *          *          *          *
AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA
TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT
 R   T   E   A   L   N   H   H   N   T   L   V   C   S   V   T>
----------------------------------------------------------------

            540        550        560        570
             *          *          *          *
GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG
CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC
 D   F   Y   P   A   K   I   K   V   R   W   F   R   N   G   Q>
----------------------------------------------------------------
```

FIG. 27B

```
580          590          600          610          620
 *            *            *            *            *
GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC
CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG
 E   E   T   V   G   V   S   S   T   Q   L   I   R   N   G   D>
-------------------------------------------------------------

  630          640          650          660          670
   *            *            *            *            *
TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA
ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT
 W   T   F   Q   V   L   V   M   L   E   M   T   P   H   Q   G>
-------------------------------------------------------------

    680          690          700          710          720
     *            *            *            *            *
GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC
CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG
 E   V   Y   T   C   H   V   E   H   P   S   L   K   S   P   I>
------------------------------------ I-Ad β-2 DOMAIN  ------

      730          740          750          760          770
       *            *            *            *            *
ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC
TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG
 T   V   E   W   T   S   G   G   G   G   S   G   G   G   G   S>
-------------><------------------ 24 AMINO ACID LINKER -----

         780          790          800          810
          *            *            *            *
GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCG AGT GAA GAC GAC ATT
CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA
 G   G   G   G   S   G   G   G   G   S   S   S   E   D   D   I>
-------------------------------------------><-------------

820          830          840          850          860
 *            *            *            *            *
GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT
CTC CGG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA
 E   A   D   H   V   G   F   Y   G   T   T   V   Y   Q   S   P>
----- I-Ad α-1 DOMAIN ------------------------------------------
```

FIG.27C

870 880 890 900 910

GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC
CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG
G D I G Q Y T H E F D G D E L F>

920 930 940 950 960

TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT
ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA
Y V D L D K K K T V W R L P E F>

970 980 990 1000 1010

GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT
CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA
G Q L I L F E P Q G G L Q N I A>

1020 1030 1040 1050

GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC
CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG
A E K H N L G I L T K R S N F T>
------------------------------------ I-Ad α-1 DOMAIN --------

1060 1070 1080 1090 1100

CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT
GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA
P A T N E A P Q A T V F P K S P>
-----------><----- I-Ad α-2 DOMAIN ---------------------------

1110 1120 1130 1140 1150

GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC
CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG
V L L G Q P N T L I C F V D N I>

FIG.27D

```
    1160              1170            1180            1190              1200
      *                 *               *               *                 *
TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC
AAG GGT GGA CAC TAG TTG TAG TGT ACC GAG TCT TTA TCG TTC AGT CAG
 F   P   P   V   I   N   I   T   W   L   R   N   S   K   S   V>
-----------------------------------------------------------------

        1210            1220              1230            1240            1250
          *               *                 *               *               *
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC
TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG
 T   D   G   V   Y   E   T   S   F   L   V   N   R   D   H   S>
-----------------------------------------------------------------

            1260            1270            1280              1290
              *               *               *                 *
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT
AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA
 F   H   K   L   S   Y   L   T   F   I   P   S   D   D   D   I>
-----------------------------------------------------------------

1300            1310              1320            1330            1340
  *               *                 *               *               *
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA
ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTT
 Y   D   C   K   V   E   H   W   G   L   E   E   P   V   L   K>
------------------------------------ I-Ad α-2 DOMAIN  --------

  1350            1360            1370              1380
    *               *               *                 *
CAC TGG TCC CGG GCT AGT CAC CAT CAC CAT CAT CAC TAG
GTG ACC AGG GCC CGA TCA GTG GTA GTG GTA GTA GTG ATC
 H   W   S   R   A   S   H   H   H   H   H   H  *>
------->&lt;------------------ 6 X HIS tag ----->
```

FIG.27E

```
          10          20          30          40          50
          *           *           *           *           *
CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG
GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC
      M   A   L   G   I   P   S   L   L   L   S   A   A   V   V>
      <---------------  I-Ad β CHAIN LEADER  ----------------

          60          70          80          90
          *           *           *           *
GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
 V   L   M   V   L   S   S   P   R   T   L   S   I   S   Q   A>
-------------------------------------------><-------------

100         110         120         130         140
 *           *           *           *           *
GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT
 V   H   A   A   H   A   E   I   N   E   A   G   R   A   S   G>
------  OVA 323-339  ------------------------------><----------

  150         160         170         180         190
   *           *           *           *           *
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
 G   G   G   S   G   G   G   G   N   S   E   R   H   F   V   V>
--  10 AMINO ACID LINKER --><------  I-Ad β-1 DOMAIN  ---------

    200         210         220         230         240
     *           *           *           *           *
CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
GTC AAG TTC CCG CTC ACG ATG ATG TCC TTG CCC TGC GTC GCG TAT GCC
 Q   F   K   G   E   C   Y   Y   T   N   G   T   Q   R   I   R>
-------------------------------------------------------------

      250         260         270         280         290
       *           *           *           *           *
CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG
 L   V   T   R   Y   I   Y   N   R   E   E   Y   V   R   Y   D>
-------------------------------------------------------------
```

FIG.28A

```
     300       310       320       330
      *         *         *         *
AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG
 S   D   V   G   E   Y   R   A   V   T   E   L   G   R   P   D>
----------------------------------------------------------------

340       350        360       370       380
 *         *          *         *         *
GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC
CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG
 A   E   Y   W   N   S   Q   P   E   I   L   E   R   T   R   A>
----------------------------------------------------------------

  390       400       410        420       430
   *         *         *          *         *
GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC
CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG
 E   V   D   T   A   C   R   H   N   Y   E   G   P   E   T   S>
----------------------------------------------------------------

   440        450       460       470        480
    *          *         *         *          *
ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC
TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG
 T   S   L   R   R   L   E   Q   P   N   V   A   I   S   L   S>
---  I-Ad β-1 DOMAIN  -><-------  I-Ad β-2 DOMAIN  ------------

     490       500        510       520       530
      *         *          *         *         *
AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA
TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT
 R   T   E   A   L   N   H   H   N   T   L   V   C   S   V   T>
----------------------------------------------------------------

        540       550       560        570
         *         *         *          *
GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG
CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC
 D   F   Y   P   A   K   I   K   V   R   W   F   R   N   G   Q>
----------------------------------------------------------------
```

FIG.28B

```
580          590          600          610          620
 *            *            *            *            *
GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC
CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG
 E   E   T   V   G   V   S   S   T   Q   L   I   R   N   G   D>
-------------------------------------------------------------

  630          640          650          660          670
   *            *            *            *            *
TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA
ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT
 W   T   F   Q   V   L   V   M   L   E   M   T   P   H   Q   G>
-------------------------------------------------------------

    680          690          700          710          720
     *            *            *            *            *
GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC
CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG
 E   V   Y   T   C   H   V   E   H   P   S   L   K   S   P   I>
---------------------------------- I-Ad β-2 DOMAIN ------

        730          740          750          760          770
         *            *            *            *            *
ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC
TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG
 T   V   E   W   T   S   G   G   G   G   S   G   G   G   G   S>
-------------><------------------ 24 AMINO ACID LINKER   ----

            780          790          800          810
             *            *            *            *
GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCG AGT GAA GAC GAC ATT
CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA
 G   G   G   G   S   G   G   G   G   S   S   S   E   D   D   I>
-----------------------------------------><-------------

820          830          840          850          860
 *            *            *            *            *
GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT
CTC CGG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA
 E   A   D   H   V   G   F   Y   G   T   T   V   Y   Q   S   P>
----- I-Ad α-1 DOMAIN ------------------------------------------
```

FIG.28C

```
   870         880         890         900         910
    *           *           *           *           *
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC
CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG
 G   D   I   G   Q   Y   T   H   E   F   D   G   D   E   L   F>
----------------------------------------------------------------

     920         930         940         950         960
      *           *           *           *           *
TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT
ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA
 Y   V   D   L   D   K   K   K   T   V   W   R   L   P   E   F>
----------------------------------------------------------------

       970         980         990        1000        1010
        *           *           *           *           *
GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT
CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA
 G   Q   L   I   L   F   E   P   Q   G   G   L   Q   N   I   A>
----------------------------------------------------------------

         1020        1030        1040        1050
           *           *           *           *
GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC
CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG
 A   E   K   H   N   L   G   I   L   T   K   R   S   N   F   T>
-------------------------------------- I-Ad α-1 DOMAIN ---------

1060        1070        1080        1090        1100
 *           *           *           *           *
CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT
GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA
 P   A   T   N   E   A   P   Q   A   T   V   F   P   K   S   P>
----------><----- I-Ad α-2 DOMAIN ------------------------------

  1110        1120        1130        1140        1150
    *           *           *           *           *
GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC
CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG
 V   L   L   G   Q   P   N   T   L   I   C   F   V   D   N   I>
----------------------------------------------------------------
```

FIG.28D

```
   1160          1170          1180          1190          1200
     *             *             *             *             *
TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC
AAG GGT GGA CAC TAG TTG TAG TGT ACC GAG TCT TTA TCG TTC AGT CAG
 F   P   P   V   I   N   I   T   W   L   R   N   S   K   S   V>
-------------------------------------------------------------

      1210          1220          1230          1240          1250
        *             *             *             *             *
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC
TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG
 T   D   G   V   Y   E   T   S   F   L   V   N   R   D   H   S>
-------------------------------------------------------------

         1260          1270          1280          1290
           *             *             *             *
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT
AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA
 F   H   K   L   S   Y   L   T   F   I   P   S   D   D   D   I>
-------------------------------------------------------------

1300          1310          1320          1330          1340
  *             *             *             *             *
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA
ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTT
 Y   D   C   K   V   E   H   W   G   L   E   E   P   V   L   K>
---------------------------------- I-Ad α-2  DOMAIN --------

 1350          1360          1370          1380          1390
   *             *             *             *             *
CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG CTG ACA GAA ACT
GTG ACC CTT GGA CTC TAA GGT CGG GGG TAC AGT CTC GAC TGT CTT TGA
 H   W   E   P   E   I   P   A   P   M   S   E   L   T   E   T>
-------><-------- I-Ad α-TM DOMAIN ----------------------------

   1400          1410          1420          1430          1440
     *             *             *             *             *
GTG GTG TGT GCC CTG GGG TTG TCT GTG GGC CTT GTG GGC ATC GTG GTG
CAC CAC ACA CGG GAC CCC AAC AGA CAC CCG GAA CAC CCG TAG CAC CAC
 V   V   C   A   L   G   L   S   V   G   L   V   G   I   V   V>
-------------------------------------------------------------
```

FIG.28E

```
      1450          1460          1470          1480          1490
        *             *             *             *             *
GGC ACC ATC TTC ATC ATT CAA GGC CTG CGA TCA GGT GGC ACC TCC AGA
CCG TGG TAG AAG TAG TAA GTT CCG GAC GCT AGT CCA CCG TGG AGG TCT
 G   T   I   F   I   I   Q   G   L   R   S   G   G   T   S   R>
-------------------------------------------------------------

CAC CCA GGG CCT TTA TGA
GTG GGT CCC GGA AAT ACT
 H   P   G   P   L   *>
- I-Ad α-TM DOMAIN ->
```

FIG.28F

```
          10          20          30          40          50
          *           *           *           *           *
CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG
GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC
      M   A   L   Q   I   P   S   L   L   L   S   A   A   V   V>
      <--------------- I-Ad β CHAIN LEADER ----------------

          60          70          80          90
          *           *           *           *
GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
 V   L   M   V   L   S   S   P   R   T   L   S   I   S   Q   A>
-------------------------------------------><--------------

100         110         120         130         140
 *           *           *           *           *
GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT
 V   H   A   A   H   A   E   I   N   E   A   G   R   A   S   G>
------ OVA 323-339 ----------------------------><----------

  150         160         170         180         190
   *           *           *           *           *
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
 G   G   G   S   G   G   G   G   N   S   E   R   H   F   V   V>
-- 10 AMINO ACID LINKER --><------ I-Ad β-1 DOMAIN ---------

    200         210         220         230         240
     *           *           *           *           *
CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC
 Q   F   K   G   E   C   Y   Y   T   N   G   T   Q   R   I   R>
-----------------------------------------------------------

      250         260         270         280         290
       *           *           *           *           *
CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG
 L   V   T   R   Y   I   Y   N   R   E   E   Y   V   R   Y   D>
-----------------------------------------------------------
```

FIG.29A

```
          300         310         320         330
           *           *           *           *
AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG
 S   D   V   G   E   Y   R   A   V   T   E   L   G   R   P   D>
-----------------------------------------------------------------

340         350         360         370         380
 *           *           *           *           *
GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC
CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG
 A   E   Y   W   N   S   Q   P   E   I   L   E   R   T   R   A>
-----------------------------------------------------------------

  390         400         410         420         430
   *           *           *           *           *
GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC
CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG
 E   V   D   T   A   C   R   H   N   Y   E   G   P   E   T   S>
-----------------------------------------------------------------

    440         450         460         470         480
     *           *           *           *           *
ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC
TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG
 T   S   L   R   R   L   E   Q   P   N   V   A   I   S   L   S>
---  I-Ad β-1 DOMAIN  -><-------  I-Ad β-2 DOMAIN  ------------

      490         500         510         520         530
       *           *           *           *           *
AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA
TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT
 R   T   E   A   L   N   H   H   N   T   L   V   C   S   V   T>
-----------------------------------------------------------------

          540         550         560         570
           *           *           *           *
GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG
CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC
 D   F   Y   P   A   K   I   K   V   R   W   F   R   N   G   Q>
-----------------------------------------------------------------
```

FIG.29B

```
580          590          600          610          620
 *            *            *            *            *
GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC
CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG
 E   E   T   V   G   V   S   S   T   Q   L   I   R   N   G   D>
-------------------------------------------------------------

  630          640          650          660          670
   *            *            *            *            *
TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA
ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT
 W   T   F   Q   V   L   V   M   L   E   M   T   P   H   Q   G>
-------------------------------------------------------------

    680          690          700          710          720
     *            *            *            *            *
GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC
CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG
 E   V   Y   T   C   H   V   E   H   P   S   L   K   S   P   I>
---------------------------------- I-Ad β-2 DOMAIN ------

       730          740          750          760          770
        *            *            *            *            *
ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC
TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG
 T   V   E   W   T   S   G   G   G   G   S   G   G   G   G   S>
------------><------------------ 24 AMINO ACID LINKER -----

          780          790          800          810
           *            *            *            *
GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCG AGT GAA GAC GAC ATT
CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA
 G   G   G   G   S   G   G   G   G   S   S   S   E   D   D   I>
-------------------------------------------><--------------

820          830          840          850          860
 *            *            *            *            *
GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT
CTC CGG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA
 E   A   D   H   V   G   F   Y   G   T   T   V   Y   Q   S   P>
----- I-Ad α-1 DOMAIN -----------------------------------------
```

FIG.29C

```
  870         880         890         900         910
   *           *           *           *           *
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC
CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG
 G   D   I   G   Q   Y   T   H   E   F   D   G   D   E   L   F>
-------------------------------------------------------------

    920         930         940         950         960
     *           *           *           *           *
TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT
ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA
 Y   V   D   L   D   K   K   K   T   V   W   R   L   P   E   F>
-------------------------------------------------------------

       970         980         990        1000        1010
        *           *           *           *           *
GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT
CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA GCT GAC GTT TTG TAT CGA
 G   Q   L   I   L   F   E   P   Q   G   G   L   Q   N   I   A>
-------------------------------------------------------------

           1020        1030        1040        1050
            *           *           *           *
GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC
CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG
 A   E   K   H   N   L   G   I   L   T   K   R   S   N   F   T>
---------------------------------- I-Ad α-1 DOMAIN --------

1060        1070        1080        1090        1100
  *           *           *           *           *
CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT
GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA
 P   A   T   N   E   A   P   Q   A   T   V   F   P   K   S   P>
----------><----- I-Ad α-2 DOMAIN -------------------------

 1110        1120        1130        1140        1150
   *           *           *           *           *
GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC
CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG
 V   L   L   G   Q   P   N   T   L   I   C   F   V   D   N   I>
-------------------------------------------------------------
```

FIG.29D

```
    1160          1170          1180          1190          1200
      *             *             *             *             *
TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC
AAG GGT GGA CAC TAG TTG TAG TGT ACC GAG TCT TTA TCG TTC AGT CAG
 F   P   P   V   I   N   I   T   W   L   R   N   S   K   S   V>
-------------------------------------------------------------

      1210          1220          1230          1240          1250
        *             *             *             *             *
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC
TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG
 T   D   G   V   Y   E   T   S   F   L   V   N   R   D   H  -S>
-------------------------------------------------------------

          1260          1270          1280          1290
            *             *             *             *
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT
AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA
 F   H   K   L   S   Y   L   T   F   I   P   S   D   D   D   I>
-------------------------------------------------------------

1300          1310          1320          1330          1340
  *             *             *             *             *
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA
ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTT
 Y   D   C   K   V   E   H   W   G   L   E   E   P   V   L   K>
---------------------------------- I-Ad α-2 DOMAIN --------

 1350          1360          1370          1380
   *             *             *             *
CAC TGG GAG GAA GAA GAG TAC ATG CCG ATG GAA TGA
GTG ACC CTC CTT CTT CTC ATG TAC GGC TAC CTT ACT

 H   W   E   E   E   E   Y   M   P   M   E   *>
------->&lt;-------- EE TAG ---------------->
```

FIG.29E

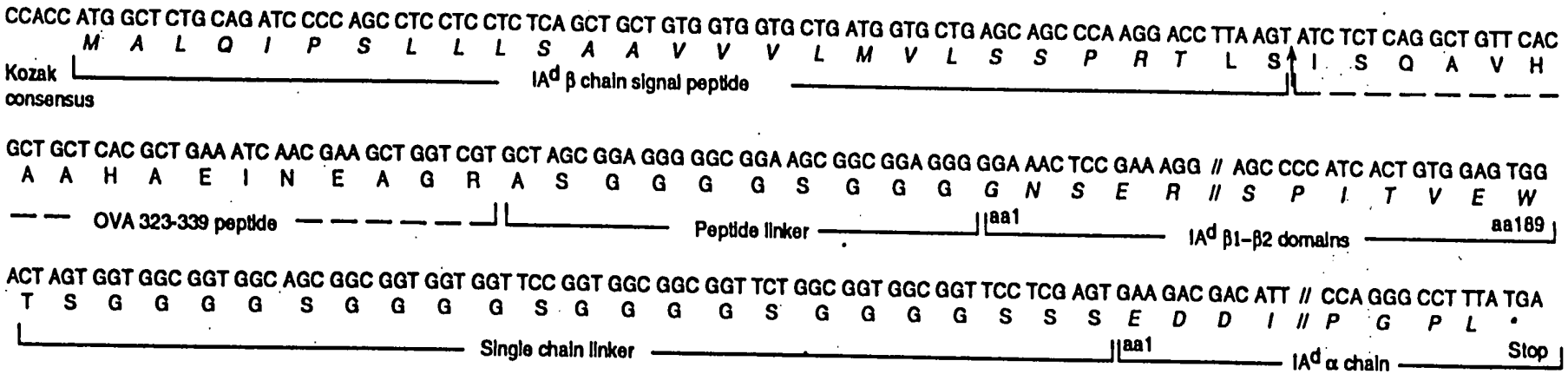


FIG. 30

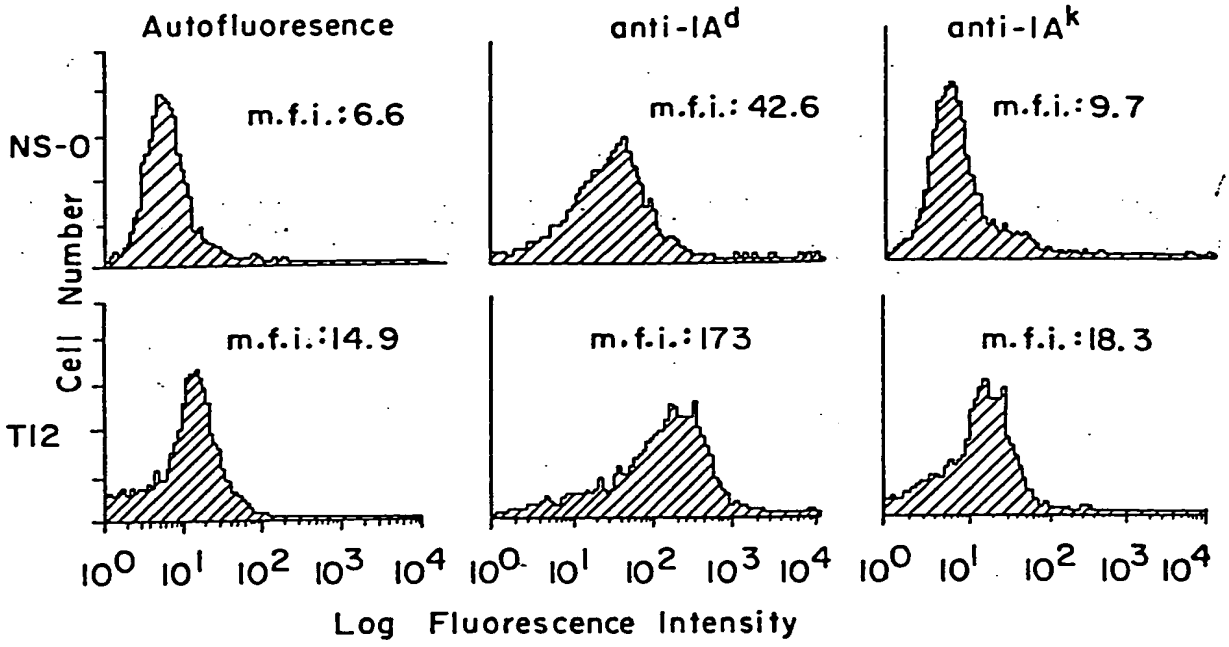


FIG. 31A

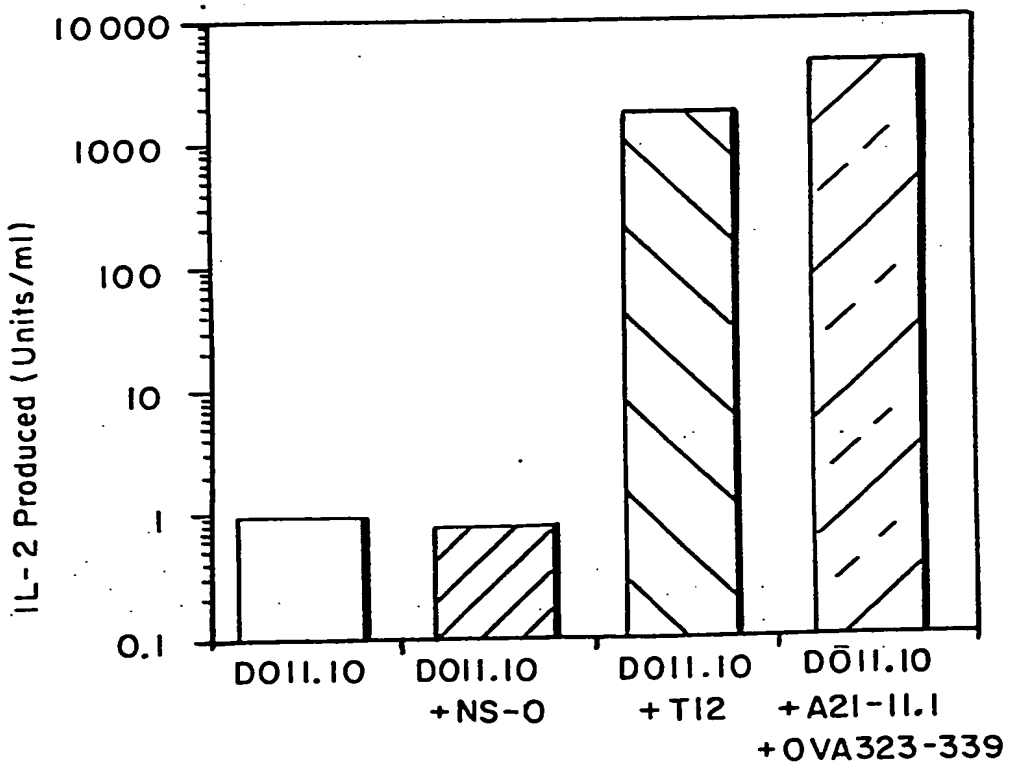


FIG. 31B

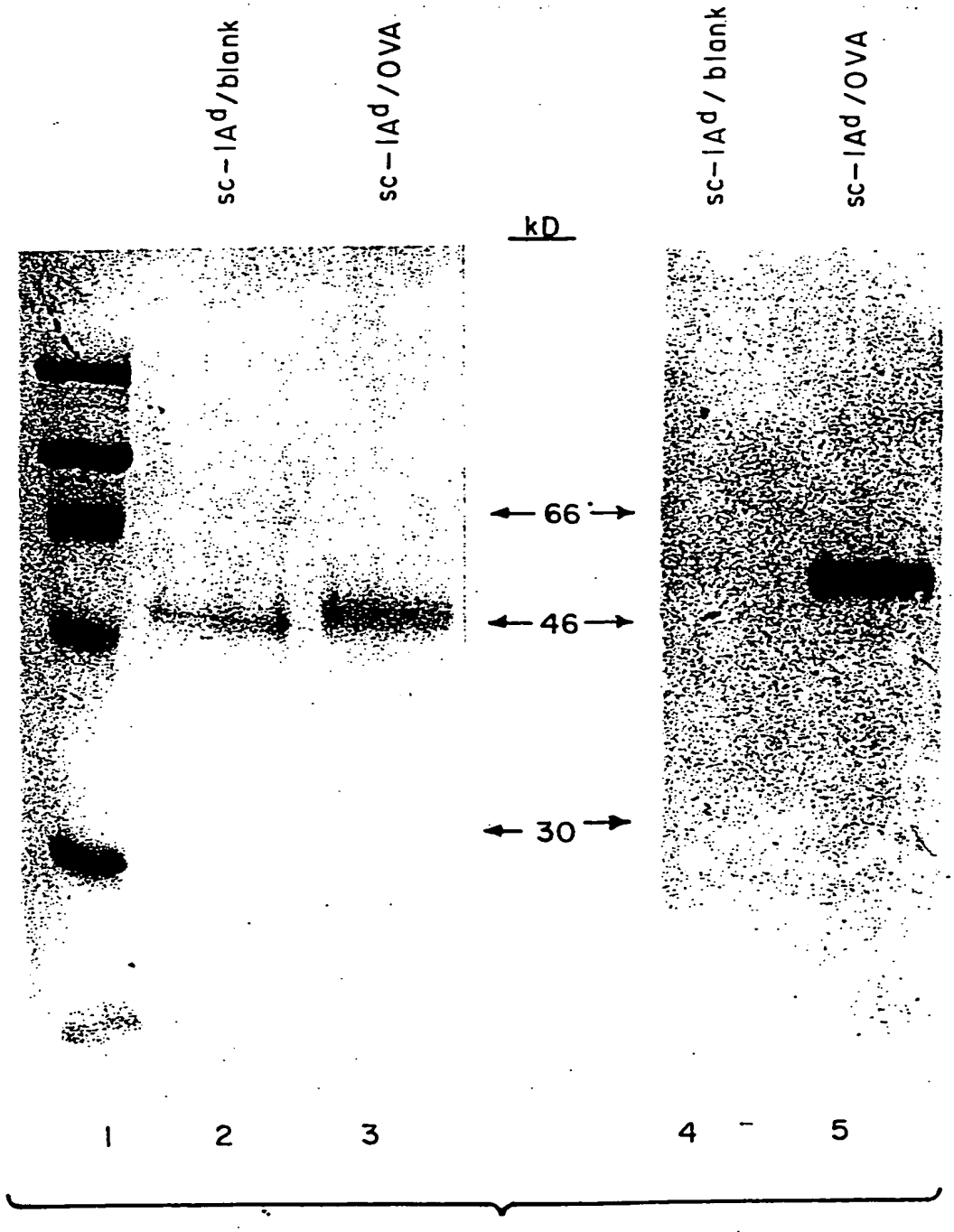


FIG.32

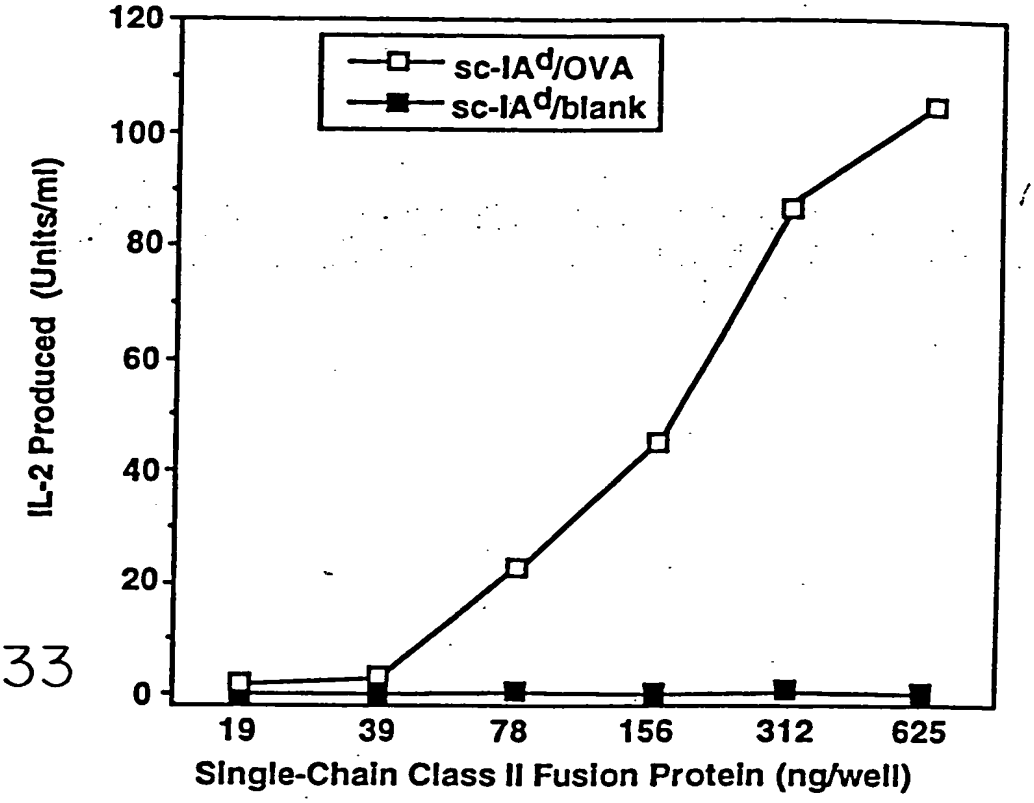


FIG.33

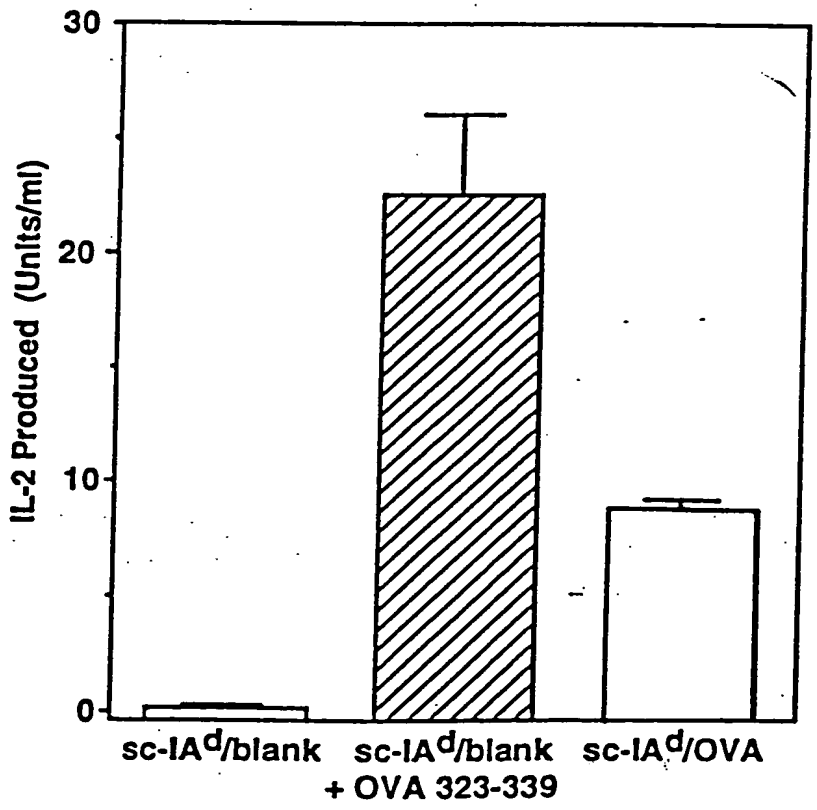


FIG.34C

FIG.34A

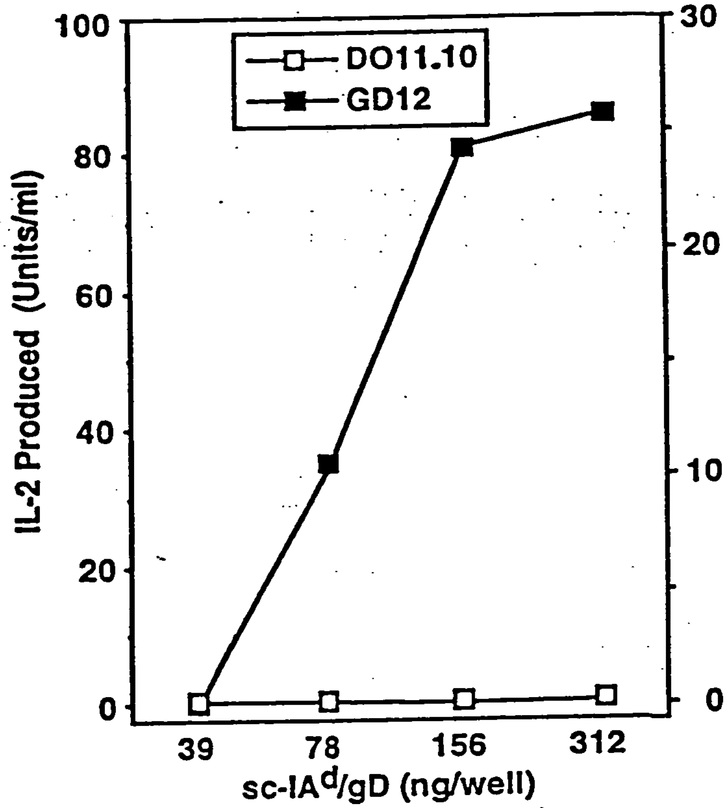
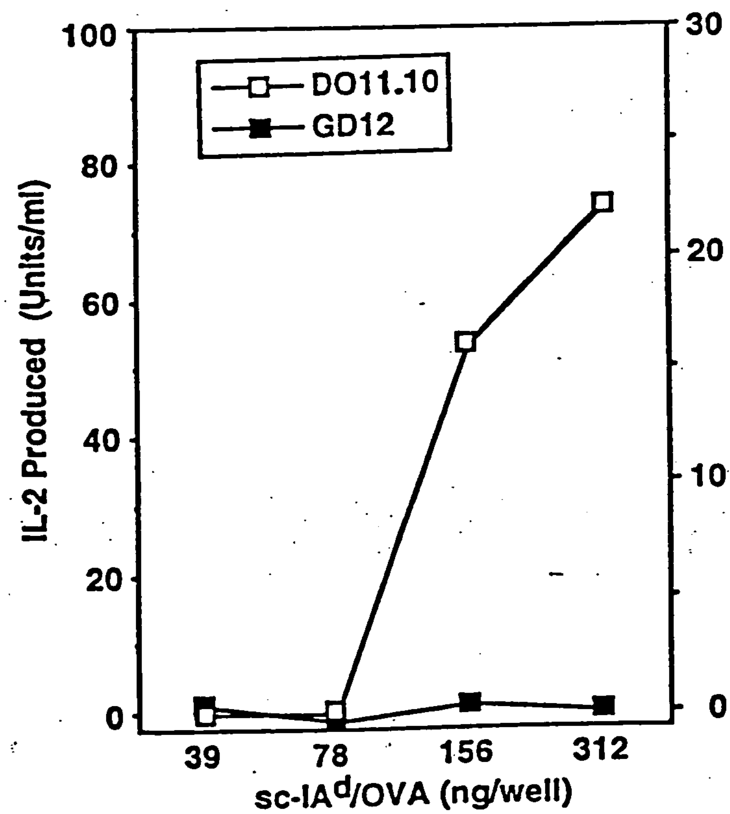


FIG.34B



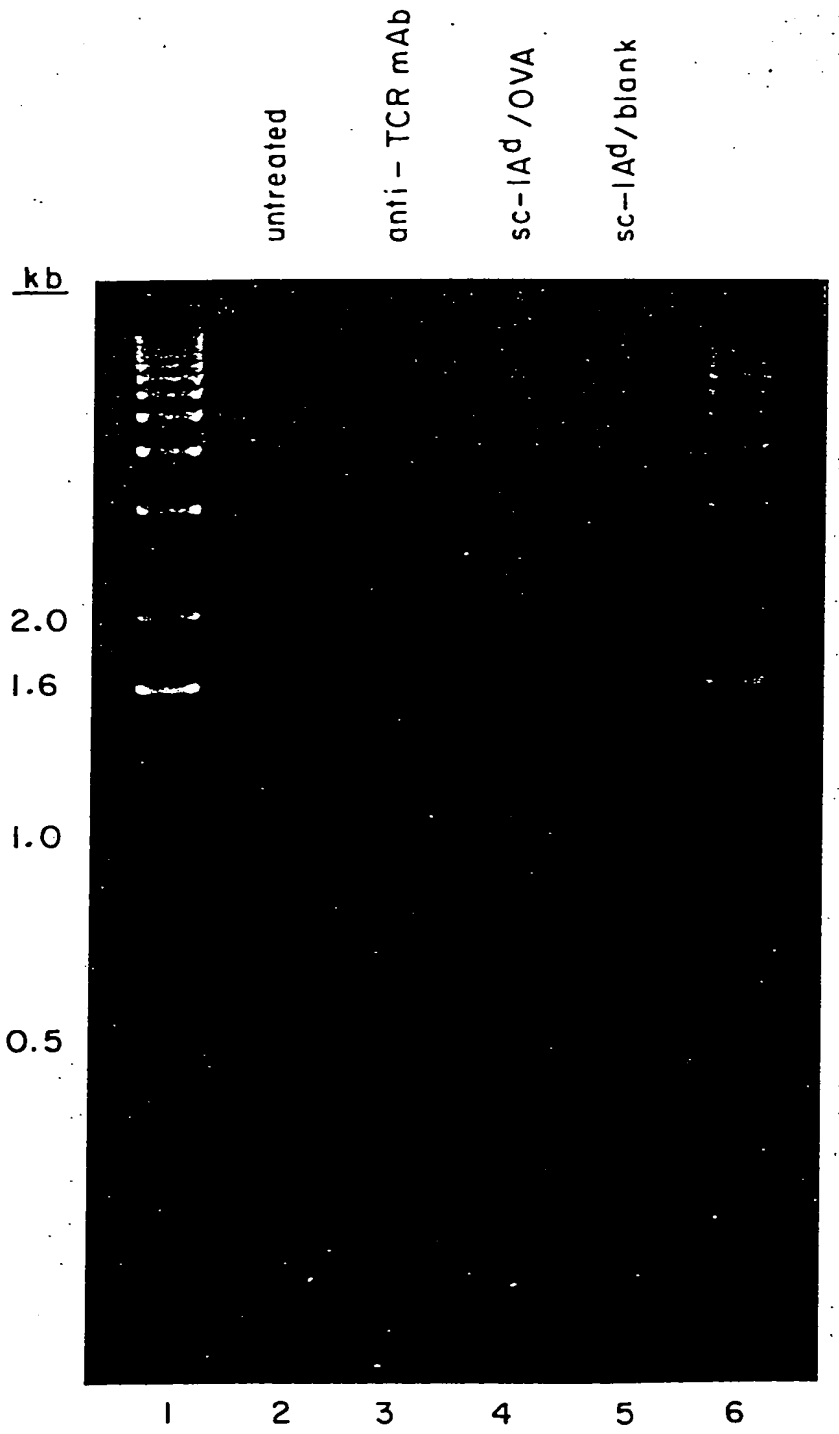


FIG. 35

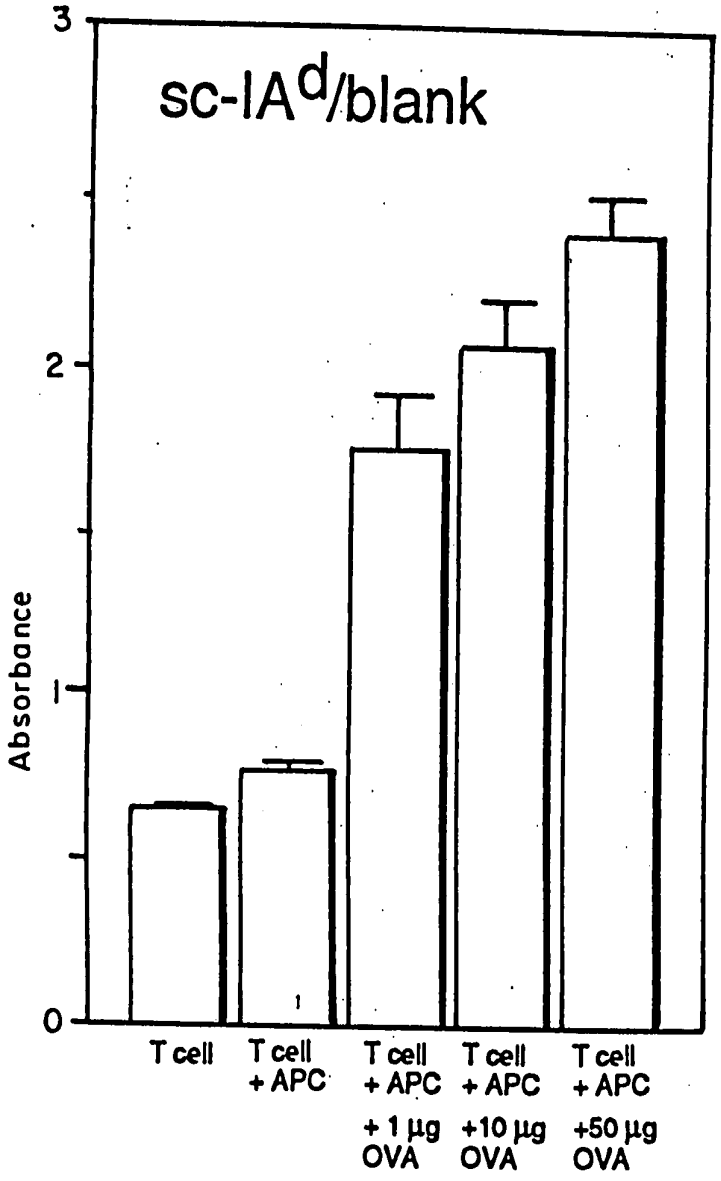


FIG. 36A

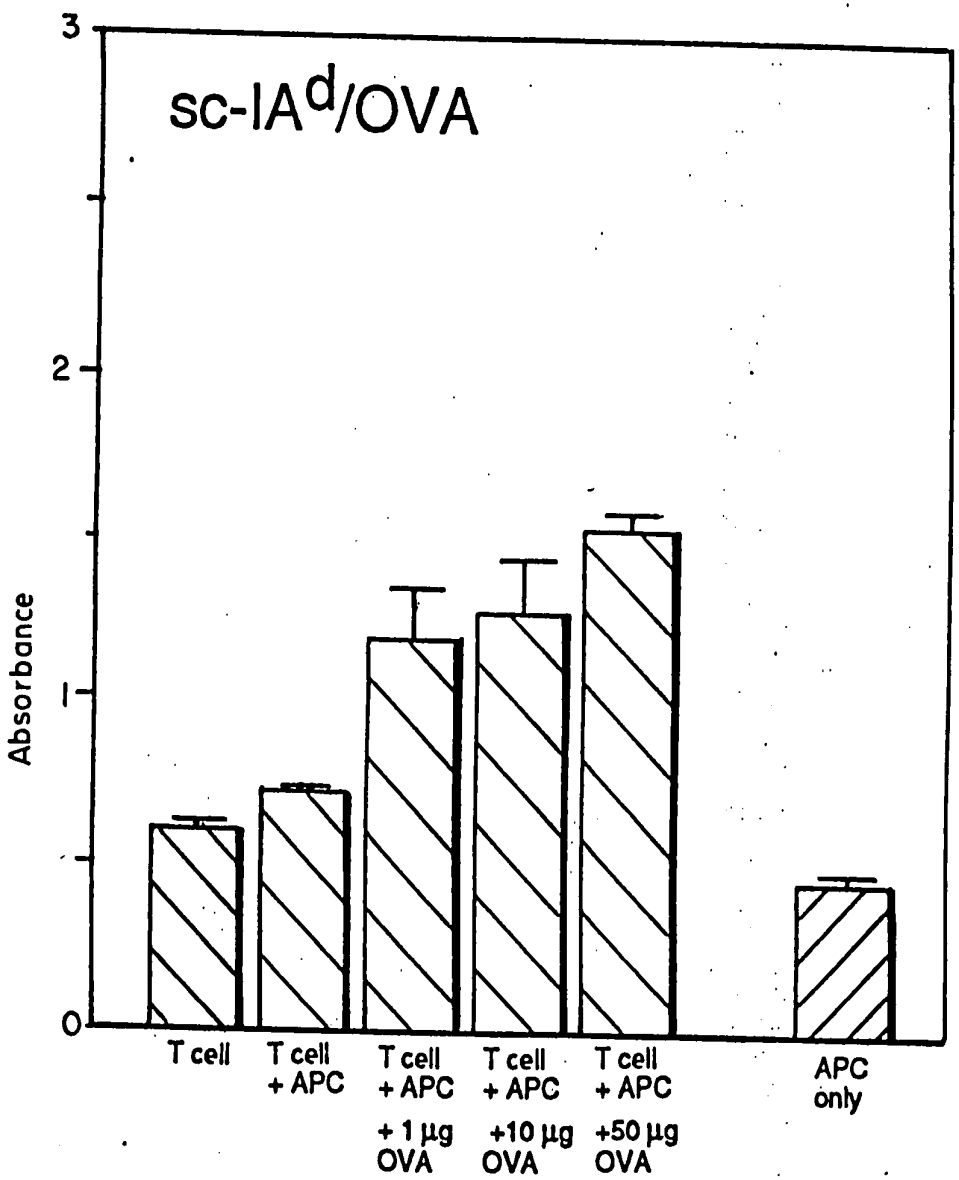


FIG. 36B